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US-10-290-072-148 US-10-290-072-148 US-10-290-072-130 US-10-290-072-130 US-10-141-531-131 US-10-141-531-184 US-10-290-072-184 US-10-290-072-112 US-10-290-072-112 US-10-290-072-112 US-10-141-531-112 US-10-290-072-121 US-10-290-072-121 US-10-290-072-121 US-10-290-072-121 US-10-290-072-121 US-10-290-072-121 US-10-290-072-166 US-10-141-531-166 US-10-141-531-166 US-10-141-531-166 US-10-141-531-166 US-10-141-531-166 US-10-141-531-166 US-10-141-531-121 US-10-141-531-121 US-10-141-531-166 US-10-141-531-120 US-10-141-531-166 US-10-141-531-166 US-10-141-531-186 US-10-141-531-186

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85, Appl 130, Appl 184, App 1112, App 1112, App 1175, App 1175, App 1175, Appl 1175, Appl 1175, Appl 1175, Appl 1171, App

Sequence Sequence

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ALIGNMENTS

us-09-825-212-1.rapb

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SEQ ID NO 1
LENGTH: 320
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Sequence 14, Appl
Sequence 14, Appl
Sequence 2, Appli
Sequence 25, Appli
Sequence 26, Appli
Sequence 10, Appli
Sequence 66, Appli
                                                                          September 15, 2004, 12:20:54 ; Search time 135 Seconds (without alignments) 760.153 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                            1662
1 MGTEIDFDIAIIGAGPAGMT......AAEXIEHLNDQARSHHHHHH 320
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-925-637-14

US-10-084-205-14

US-10-10-14-2-14

6 US-10-712-713-14

6 US-10-787-887-2

4 US-10-787-887-2

6 US-10-787-887-2

1 US-10-290-072-66

4 US-10-141-531-66

4 US-10-032-201B-398

4 US-10-032-201B-398

5 US-10-290-072-103

6 US-10-141-531-103

7 US-10-141-531-103

8 US-10-141-531-103
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       1335176 seqs, 320689617 residues
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                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Maximum DB
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Sequence 1, Application US/09825212
; Sequence 1, Application US/09825212
; Publication No. US20030166843A1
; GENERAL INFORMATION:
; APPLICAMT: Benson, Timothy E
; TITLE OF INVENTION: STRAHYLOCOCCUS AUREUS THIOREDOXIN REDUCTASE
; TITLE OF INVENTION STRAHYLOCOCCUS AUREUS THIOREDOXIN REDUCTASE
; TITLE PEPERENCE: 00032.US1
; CURRENT APPLICATION NUMBER: US/09/825,212
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,055
; RIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: RatentIn Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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; ORGANISM: Staphylococcus aureus
US-09-825-212-1
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Best Local Similarity 100.
Matches 320; Conservative
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TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REPERENCE: PBS60
CURRENT APPLICATION NUMBER: US/09/925,637
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 1990-09-01
PRIOR FILING DATE: 1997-01-03
PRIOR PLICATION NUMBER: US 08/781,986
PRIOR FILING DATE: 1997-01-02
PRIOR FILING DATE: 1997-01-02
PRIOR FILING DATE: 1997-01-06
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 14
LENGTH: 312
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                                                              MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS
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Pred. No. 1.7e-141;
0; Mismatches 2;
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                                                                                                                                             301 AAEYIEHLNDQARSHHHHHH 320
                                                                                                                                                                      301 AAEYIEHLNDQARSHHHHHH 320
                                                                                                                                                                                                                                                                                    , Sequence 14, Application US/09925637
, Patent No. US20020103338A1
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Best Local Similarity 99.4%;
Matches 310; Conservative
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US-09-925-637-14
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NESULY 4

Sequence 14, Application US/10712713

Publication No. 220040082002A1

GENERAL INFORMATION:

APPLICANT: Choi, Gil

TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides

TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides

TITLE REFERENCE: PB515F1

CURRENT FILING DATE: 2003-11-14

CURRENT FILING DATE: 2003-11-14

PRIOR PPLICATION NUMBER: US/10/084,205

PRIOR PPLICATION NUMBER: PCT/US00/23773

PRIOR APPLICATION NUMBER: 60/151,933

PRIOR APPLICATION NUMBER: 60/151,933

NUMBER: OF SEQ ID NOS: 74
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APPLICANT: Choi, Gil
TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
FILE REPERENCE: PBELSOH
CURRENT APPLICATION NUMBER: US/10/084,205
CURRENT APPLICATION NUMBER: US/202-02-8
PRIOR APPLICATION NUMBER: PCT/US00/23773
PRIOR PLING DATE: 2000-08-31
PRIOR PLING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 14
LENGTH: 312
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Pred. No. 1.7e-141;
                                                                                                                                                                                                                                                                                                                                                                                               Score 1593; DB 14;
Pred. No. 1.7e-141;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Staphylococcus aureus
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99.4%;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.8%;
Best Local Similarity 99.4%;
Matches 310; Conservative
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SEQ ID NO 14
LENGTH: 312
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Best Local Similarity
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APPLICANT: Van Rooijen, Gijs
APPLICANT: Van Rooijen, Gijs
APPLICANT: Deckers, Harm
APPLICANT: Beckers, Harm
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Applicants, Steve
APPLICANT: Moloney, Maurice
ITLE OF INVENTION: MTHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
ITLE OF INVENTION: COMPOSITIONS
FILE REPRENCE: 38814 3518
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 265
BENOTH 311
           243 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                            DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
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Pred. No. 1.7e-138;
1; Mismatches 5;
                                                                                                                                                                                      Sequence 265, Application US/10032201B; Publication No. US20030167524A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10787887; Publication No. US20040161809A1; GENERAL INFORMATION:
APPLICANT: Aharonowitz, Yair; APPLICANT: Borovok, Ilya; APPLICANT: Cohen, Gerald; APPLICANT: Uziel, Orit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Staphylococcus aureus
US-10-032-201B-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9%;
98.1%;
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Best Local Similarity 98.1:
Matches 304; Conservative
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                                                                                                                VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 180
                                                                                                                                                                                 RAQRILQDRAFKNDKIDFIWSHTTKSINBKDGKVGSVTLTSTKDGSBETHEADGVFIVIG 240
                                                                                                                                                                                                                                                   MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300
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                                                 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
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CURRENT APPLICATION NUMBER: 05.10/787,887
CURRENT FILING DATE: 10.04-02-27
PRIOR APPLICATION NUMBER: US 60/076,525
PRIOR APPLICATION NUMBER: US 90/261,301
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
RIOR FILING DATE: 1999-03-02
RIOR FILING DATE: 1999-03-02
ROBERT OF SEQ ID NOS: 10
SOFFWARE: PatentIn version 3.2
SEQ ID NO 2
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Pred. No. 1.8e-140;
0; Mismatches 2; Indels 0
      Indels
     2,
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10787887
Publication No. US20040161809A1
GENERAL INFORMATION:
APPLICANT: Abaronowitz, Yair
APPLICANT: Borovok, Ilya
APPLICANT: Cohen, Gerald
APPLICANT: Uziel, Orit
APPLICANT: Katz, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-787-887-2
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310; Conservative
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Matches 308; Conservative
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APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: Designation, John R.
APPLICANT: Designation, John R.
APPLICANT: Designation, John R.
APPLICANT: Heaffetz, Peter
APPLICANT: Heaffetz, Peter
APPLICANT: Muchhal, 10meh
TITLE OF INVENTION: NUMBER: US, 10/141,531
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US, 60/370,609
PRIOR APPLICATION NUMBER: US, 60/289,029
PRIOR APPLICATION NUMBER: US, 60/289,029
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin Version 3.1
SEQ ID NO 66
SEQ ID NO 66
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Best Local Similarity 71.4%; Pred. No. 3.9e-100;
Matches 220; Conservative 33; Mismatches 55;
                                                                                         ; Score 1154; DB 12;
; Pred. No. 3.9e-100;
33; Mismatches 55;
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                                                                                              Query Match 69.4%;
Best Local Similarity 71.4%;
Matches 220; Conservative 3
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; ORCANISM: Bacillus subtilis
US-10-141-531-66
                   TYPE: PRT ORGANISM: Bacillus subtilis
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US-10-290-072-66
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APPLICANT: Briggs, Steven P.

APPLICANT: Briggs, Steven P.

APPLICANT: Dalmia, Bipin K.

APPLICANT: del Val, Greg

APPLICANT: del Val, Greg

APPLICANT: Heifetz, Peter

APPLICANT: Luginbuhl, Peter

APPLICANT: Luginbuhl, Peter

APPLICANT: Luginbuhl, Peter

APPLICANT: Muchhal, Umesh

TILE REFERENCE: A.71457-3

CURRENT APPLICATION NUMBER: US 60/370,609

PRIOR FILING DATE: 2002-04-05

PRIOR PLICATION NUMBER: US 60/370,609

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-05-06

PRIOR FILING DATE: 2002-05-06

PRIOR FILING DATE: 2002-05-06

PRIOR FILING DATE: 2002-05-06

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 239

SOFTWARE: Patentin version 3.2
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                   TITLE OF INVENTION: Recombinant Staphylococcus Thioredoxin Reductasse FILE REFERENCE: 85189-899
CURRENT APPLICATION NUMBER: US/10/787,887
CURRENT FILING DATE: 2004-02-27
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR PLICATION NUMBER: US 09/261,301
PRIOR FILING DATE: 1999-03-02
NUMBER OF SEC ID NOS: 10
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87.4%; Score 1452; DB 16; Length
Best Local Similarity 89.9%; Pred. No. 3.2e-128;
Matches 277; Conservative 18; Mismatches 13; Indels
                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Staphylococcus epidermidis US-10-787-887-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66, Application US/10290072 Publication No. US20030211511A1 GENERAL INFORMATION:
                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.2
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DYITELKD 309
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LENGTH: 310
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APPLICANT: Use Cockers, Harm
APPLICANT: Deckers, Harm
APPLICANT: Deckers, Harm
APPLICANT: Deckers, Harm
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bpin Kumar
APPLICANT: Dalmia, Bpin Kumar
APPLICANT: Dalmia, Steven
APPLICANT: Dalmia, Steven
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 38814 351B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT APPLICATION NUMBER: US/10/032,201B
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 235
LENGTH: 315
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APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Delmia, Bipin K.
APPLICANT: Delal Gree
APPLICANT: Desiarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Hoifetz, Peter
APPLICANT: Hoifetz, Deter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
CURRENT APPLICATION NUMBER: US/10/290,072
CURRENT FILING DATE: 2002-11-06
PRIOR FILING DATE: 2002-04-05
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68.6%; Pred. No. 2.5e-99;
ive 38; Mismatches 60
                              Sequence 235, Application US/10032201B; Publication No. US20030167524A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 103, Application US/10290072 Publication No. US20030211511A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-032-2018-235
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Best Local Similarity 68.6%
Matches 216; Conservative
                 JS-10-032-201B-235
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APPLICANT: Van Rooijen, Gijs
APPLICANT: Deckers, Harm
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Zapladhinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: MURBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
                                LGGRGVSYCAVCDGAFFRGKELVVVGGGDSAVEEGVYLTRFASKVTIVHRRDKLRAQSIL 185
                                                                       187 ODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSBETHBADGVFIYIGMKPLTA 246
                                                                                              LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
                                                                                                                                                247 PFKDLGIINDVGYIVIKDDMTISVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEXIE 306
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                                                                                                                                                                                                                                                                                                                                                    ; Sequence 198, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Bacillus subtilis
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Best Local Similarity 71.4<sup>i</sup>
Matches 220; Conservative
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306 ELQETLKT 313
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306 ELQETLKT 313
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APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: Desigration K.
APPLICANT: Desigration K.
APPLICANT: del Val, Greg
APPLICANT: Heifetz, Peter
APPLICANT: Heifetz, Peter
APPLICANT: Luginbuhl, Peter
APPLICANT: Muchhal, Umesh
TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
FILE REFERENCE: A-71457-2/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/141,531
CURRENT PILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PATENTIN version 3.1
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70.1%; Pred. No. 2.8e-99;
tive 33; Mismatches 61;
                                                                                                           Score 1145; DB 12;
Pred. No. 2.8e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Bacillus subtillis variant US-10-141-531-103
                                                ; OTHER INFORMATION: Bacillus subtillis variant US-10-290-072-139
                                                                                                             Query Match
68.9%; Score 1145; D
Best Local Similarity 70.1%; Pred, No. 2.8e
Matches 220; Conservative 33; Mismatches
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TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 70.1%
Matches 220; Conservative
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Sequence 139, Application US/10290072
Publication No. US20030211511A1
GENERAL INFORMATION:
APPLICANT: Baligas, Steven P.
APPLICANT: Dalmia, Bipin K.
APPLICANT: Desjarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Luginbuhl, Peter
APPLICANT: Muchhal, Umesh
TITIE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
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Best Local Similarity 70.1%; Fred. No. 2.8e-99;
Matches 220; Conservative 33; Mismatches 61;
                                                                                                                                                                                                                                                                    OTHER INFORMATION: Bacillus subtillis variant
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CURRENT APPLICATION NUMBER: US/10/290,072
CURRENT FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: US 60/376,609
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
SPRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PatentIn version 3.2
LENGTH: 316
  PRIOR APPLICATION NUMBER: US 60/376,682
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 10/141,531
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 239
SEQ ID NO 103
LENGTH: 316
                                                                                                                                                                                                                               ORGANISM: Artificial sequence
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US-10-290-072-139
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Sequence 139, Application US/20141531

Sequence 139, Application No. US203010074341

Sequence 139, Application No. US203010074341

APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Desjarlais, John R.
APPLICANT: Desjarlais, John R.
APPLICANT: Heifetz, Peter
APPLICANT: Muchhal, Umesh

ITILE OF INVENTION: Muchhal, Umesh

TILE REFERENCE: A-71457-2/RFT/RMS/RMK

CURRENT FILING DATE: 2002-05-06

PRIOR PRINK APPLICATION NUMBER: US 60/370,609

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PatentIn version 3.1

LENGTH: 316
                                                           VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 180
                                                                                                                       181 RAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIG 240
GPDLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
                      MKPLTAPFKDLGIINDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300
                                                                                                                                                                                                       61 GPELSNKWFEHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPDLSTKWFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Bacillus subtillis variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                      301 AAEYIEHLNDQARS 314
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Matches 220; Conservative
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US-10-141-531-139
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Db 241 MLPLSKPFENLGITNBEGYIETNDRMETKVEGIFAAGDIREKSLRQIVTATGDGSIAAQS 300
QY 301 AAEYIEHLNDQARS 314
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Db 301 VQHYVEELQETLKT 314

Search completed: September 15, 2004, 12:32:46
Job time: 136 Secs
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

September 15, 2004, 12:16:13; Search time 32 Seconds (without alignments) 516.260 Million cell updates/sec Run on:

US-09-825-212-1

Perfect score:

1 MGTEIDFDIAIIGAGPAGMT......AAEYIEHLNDQARSHHHHHH 320 BLOSUM62 Gapop 10.0 , Gapext Scoring table: Sequence:

389414 seqs, 51625971 residues

389414 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 DB DB Minimum I Maximum I

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:* Issued Patents AA:* 1 2 E 4 5 9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		40			SUMMARIES		
Result No.	Score	Query	Length	DB	ID	Description	
н	1083	5	, ц,	4	-001C-551	;	
2	940	9	П	4	-09-134	777	
æ	618	۲.	_	4	-09-328-352-8114	000	
4	607	Ġ	(A	4	09-328-352-567	, FTT0	
5	594	35.7	311	4	-09-198-452A-3	22.00	
9	ß	۵.	ന	4	-09-543-6	equence	
7	579.5	34.9	ന	4	-09-598-747-25		
ထ	575	4	0	4	-09-598-747-7	Semience 25, Appl	
σ	571.5	34.4	\sim	4	-09-134		
10	569.5	4.	\sim	4	-09-540-014-25	Semience 3637, Apr	
11	568.5	34.2	⋖	4	0	Seguence 23, Appi	
12	559	33.6	\sim	4	09-540-014-24	Semience 12036, A	
13	549.5	3	∼	4	-252-991	Semience 24, Appl	
14	524.5		ന	4	09-540-014-9	Semience 27047, A	
15	13	0	\sim	Н	-08-386-	, ,	
16	497.5	29.9		4	19-598-747-2	- [
17	484.5	g	\circ	4	9-598-747-6	V 4	
18	482	9	$\overline{}$	-	JR-220-6	Sequence 8, Applia	
19	455	27.4	\sim	4	-09-252-991A-	Sequence 2, Appli	
20	454	27.3	\sim	4	-09-328-352-6394	200	
21	454	~	\sim	4	06-308-360-630	4000	
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0 0	4.	n o	~	4	9-543-681A-44	4490	
9 10	369.5	22.2	87	4	-09-134-001C-54	5497	
7 7	00.	20	339	4	US-09-107-532A-6420	Sequence 6420, Ap	

RESULT 2 US-09-134-000C-5514 ; Sequence 5514, Application US/09134000C

249 ELKD 252

Seguence 31441. A	Segmence 31700 A				Semionac 34 April	Segrence 14, Appr	Segmence 40, appl	, ,	Segmence 90 Appl	,	27.7						Sequence 32853. A	
US-09-252-991A-31441	US-09-252-991A-31700	US-09-489-039A-13402	US-09-134-001C-2974	US-09-134-0000-5068	US-09-091-097-34	US-09-091-097-10	US-09-556-877-90	US-09-620-412C-90	US-09-410-568-90	US-09-598-419-90	US-09-328-352-6168	US-09-252-991A-28041	US-09-262-856A-5	US-09-134-001C-3405	118-09-252-6618-25692	20 C2 - MICC 202 C0 C11	US-09-252-991A-32853	US-09-543-681A-5905
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17.2	16.8	16.4	15.2	14.3	14.1	14.0	13.5	13.5	13.5	13.5	13.1	12.9	12.8	12.6	12.6	10.3	7.7	12.0
285.5	279	273	253	238	234	233	225	225	225	225	218.5	215	212	210	210	200	101	199
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	1 1	45

ALIGNMENTS

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Sequence 5512, Application US/09134001C
Patent No. 6380370
GERREAL INFORMATION:
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GERREAL INFORMATION:
GERREAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PELLOR PAPPLICATION NUMBER: US 60/064,964
PRIOR PELLOR DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                65.2%; Score 1083; DB 4;
85.7%; Pred. No. 5.5e-100;
tive 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209; Conservative
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Best Local Similarity
Matches 209; Conserv
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US-09-134-001C-5512
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Sequence 5678, Application US/09328352

Fatent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 DRAF---KNDKIDFIWSHTIKSINEKDGKVGSVTLISIKDGSEETHEADGVFIYIGMKPL 244
                                                                                                                                                                188 DHLFVKEKEGKISIIWNHEVEEVLGDNTGVTSVRLKSTQDESKQDVEVHQLFVALGYKFN 247
                                                                                                                                                                                                                 245 TAPFKDLGITNDVGYIVTKDDMT----TSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ 299
                                                                                                                                                                                                                                      248 TGMF-DGQLNLRDGYIQVQSGTSGNATATSVAGVFAAGDVADSIYRQAITSAGSGCMAAL 306
                                                                                                        187
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MFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQEL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 MFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQEL
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                               68 MOAHAERFGTELVYDHINEVDLNVRPFVLKGDMEEYTCDALIIATGATAQYLGLESEQNF
                                                                     128 GGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRILQ
                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.5%; Score 607; DB 4; Length 320
43.4%; Pred. No. 2.4e-52;
tive 55; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 331, Application US/09198452A Sequence No. 6559294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Acinetobacter baumannii
US-09-328-352-5678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 134; Conservative
                                                                                                                                                                                                                                                                                              300 SAAEYIEHLND 310
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US-09-198-452A-331
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US-09-328-352-5678
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Best Local S
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTOS-0-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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       Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: LYND DOUGETE-Stamm et al
APPLICANT: LYND DOUGETE-STAMM et al
APPLICANT: LYND NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BNTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
SPRIOR FILING DATE: 1997-08-15
SUPTWARE: PATENT OF SEQ ID NOS: 6812
SOFTWARE: PATENT VEFSION 3.1
SEQ ID NO 5514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 IAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPGF-EMITGPDLSTK 67
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37.2%; Score 618; DB 4; Length 317;
Best Local Similarity 44.1%; Pred. No. 1.9e-53;
Matches 137; Conservative 53; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                   Length 310;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                   56.6%; Score 940; DB 4; ilarity 58.9%; Pred. No. 1.4e-85; Conservative 42; Mismatches 82.
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                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HL 308
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US-09-328-352-8114
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LQDRAFKNDKIDFIWSHTTKSINE---KDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
                  MPQHAEKFNTEIISDHINKVDLKNRPFRL--FGDEQEYTCDALIIATGASARYIGLPSEE 146
                                                                               266
                                                                                                                                                                                                 243 PLTAPFKDLGITNDVGYIV----TKDDMT-TSVPGIFAAGDVRDKGLRQIVTATGDGSIA 297
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/09598747
Patent No. 6531648
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lanahan, Michael B.
APPLICANT: Gasdaska, Pamela Y.
TITLE OF INVENTION: THEREIN
TITLE OF INVENTION: THEREIN
TITLE OF INVENTION: THEREIN
CURRENT APPLICATION NUMBER: US/09/598,747
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                  BLGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEBGTFTTKFADKYTIVHRRDELRAQRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GEQE-LGG---RGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 IAIIGAGPAGMTAAVYASRANLKTVMIERGI-----PGGQMANTEEVENFPGF-EMITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 ADGVFIYIGMKPLTAPFKDLGITNDV-GYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVT
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43.5%; Pred. No. 1.4e-49;
tive 50; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Arabidopsis thaliana
US-09-598-747-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 43.5
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                           326 ALDAERYLDAL 336
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PRILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                            35.7%; Score 594; DB 4; Length 311; 46.1%; Pred. No. 4.5e-51;
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                                                                                                                                                                                                                                                                                               42; Mismatches 113; Indels
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Patent No. 6605709
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                                                                                                                                                                                  TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.1
Matches 141; Conservative
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LENGTH: 339
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3897
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GENERAL INFORMATION:
APPLICANT: Lanchan, Michael B.
APPLICANT: Desai, Nalini M.
APPLICANT: Desai, Nalini M.
APPLICANT: Gaddaska, Pamela Y.
TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USFFUL
TITLE OF INVENTION: THEREIN
FILLE REFERENCE: A.31383H.
CURRENT APPLICATION NUMBER: US/09/598,747
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 42
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                                                                                                                                                                                                                                                                                                                                  Query Match

34.6%; Score 575; DB 4; Length 30
Best Local Similarity 43.2%; Pred. No. 3.4e-49;
Matches 130; Conservative 53; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3897, Application US/09134000C
Patent No. 6617156
                                                                                                                                                                                                                                                            TYPE: PRT CRGANISM: Archaeoglobus fulgidus US-09-598-747-7
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Best Local Similarity
Matches 120; Conserv
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                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 LRAQRILQDRAFKNDKID--FIMSHTTKSINEKDGK---VGSVTLTSTKDGSE-ETHBAD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
                                                                                                                                                                                                                                                                                                                                                                         123 GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
                                                                                                                                                                                                                                             183 QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEAD-----GVFI 237
                                                                                                                                                                                                                                                                              238 YIGMKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIA 297
                                                63 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                           82 ELMEEMRIQAQDFGVAFTNDEIIDVDFSQTIKTVQSASQTYQAYAVLIATGASARKIGFP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGPDLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 TEBIYDLIIIGGGSAALSAGIYAGRAMMDTLIIEKDKIGGQVTTTSBIVNYPAIRHTTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Cho, Myeong-Je
APPLICANT: Cho, Myeong-Je
APPLICANT: Caillau, Maxime
APPLICANT: Lemauz, Peggy G.
APPLICANT: Lemauz, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: NADP-Thioredoxin Reductase
FILE OF INVENTION: NADP-Thioredoxin Reductase
FILE PREBRENCE: 2001-0701.30
CURRENT APPLICATION NUMBER: US/09/540,014
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEG ID NOS: 51
SOFTWARE: FRESESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.3%; Score 569.5; DB 4; Best Local Similarity 42.1%; Pred. No. 1.3e-48; Matches 136; Conservative 55; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 25, Application US/09540014; Parent No. 6380372; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Escherichia coli
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 DISTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 ELTDKFRKQSERFGTTIFTETVTKVDFSSKPFKLFTDSKAILADAVILAIGAVAKWLSFV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 GEQE-LGG---RGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEEGTFTTKFADKYTIVHR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 RDELRAQRILQDRAFKNDKIDFIWSHTTKSINEK--DGK---VGSVTLTSTKDGSEETHE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 ADGVETYIGMKPLTAPFKDLGITNDV-GYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                           9 IAIIGAGPAGWTAAVYASRANLKTVMIERGI-----PGGQMANTEEVENFPGF-EMITGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 IAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGF-EMITGPDLSTK
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                                                                                                                                                                                                                                                                                                                                                            Query Match
33.6%; Score 559; DB 4; Length 332;
Best Local Similarity 43.2%; Pred. No. 1.5e-47;
Matches 139; Conservative 49; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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40.3%; Pred. No. 1.3e-46;
live 54; Mismatches 121;
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOUTHWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 29849, Application US/09252991A; Patent No. 6551795
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 ATGDGSIAAQSAAEYIEHLNDQ 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 AAGTGCMAALDAEHYLQEIGSQ 327
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                                                                                                                                                                                                                                                                           TYPE: PRT CRGANISM: Arabidopsis thaliana US-09-540-014-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 124; Conserv
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US-09-252-991A-29849
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US-09-252-991A-29849
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                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                      60 IGPDLSTKMFEHAKKFGAVYQYGDIKSVE------DKGBYKVINFGNKELFAKAVI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 İGPLIMERMHEHAAKFETEIIFDHISRVDLONRPFRLTGDSGEY-----TCDALI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 IATGAEYKKIGVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFAD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 KVTIVHRRDELRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGK---VGSVTLTSTKDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-ETHEADGVFIYIGMKPLTAPFK-DLGITNDVGYIVTKDDM-----TTSVPGIFAAGDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 568.5; DB 4; Length 40.7%; Pred. No. 1.9e-48; Ive 51; Mismatches 114; Indels
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APPLICANT: Del Val, Greg
APPLICANT: Del Val, Greg
APPLICANT: Lemauz, Peggy G.
APPLICANT: Lemauz, Peggy G.
APPLICANT: Bornanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thioredoxin and
TITLE OF INVENTION: NADP-Thioredoxin Reductase
FILE REFERENCE: 2001-0701.30
CURRENT APPLICATION NUMBER: US/09/540,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 RDKGLRQIVTATGDGSIAAQSAAEYIEHLNDQAR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 MDHIYRQAITSAGTGCMAALDAERYLDGLADACK 349
          GVFIYIGMKPLTAPFK-DLGITNDVGYIVTKDDM-
                                                                                                                                                                                                                                      Sequence 12096, Application US/09489039A
Patent No. 6610836
                                                                                         288 VTATGDGSIAAQSAAEYIEHLND 310
                                                                                                                   Sequence 24, Application US/09540014
Patent No. 6380372
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.78
Matches 136; Conservative
                                                                                                                                                                                                RESULT 11
US-09-489-039A-12096
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An oxido reductase enzyme system obtainable from P. chrysogenum, the set of genes enzyme encoding the same and the use of oxido reductase enzyme systems or genes encoding the same for increasing antibiotic production
                                                 250 FPAIGHEPATKFINGQLELHADGYVATKPGSTHTSVEGVFAAGDVQDKKYRQAITAAGSG 309
                                236 FIYIGMKPLTAPFKDLGITNDVGYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVTATGDG 294
193 RASKIMQARALSNPKIQVVWD---SEVVEAYGGAGGPLAGVKVKNLVTGEVSDLQVSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/386,729A FILING DATE: 10-FRB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFRENCE/DOCKET NUMBER: GBRO-024/02US
TELECOMUNICATION:
TELEPHONE: (415) 926-6200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/274,043
FILING DATE: 12-JULY-1994
APPLICATION NUMBER: US 07/820,688
FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/NL91/000101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Weil, Gotshal & Manges
2882 Sand Hill Road, Ste. 280
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APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    Aharonowitz, Yair
Van Der Voort, Lucia H.
Cohen, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
CMEDITER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    Bovenberg, Roelof A. L. Schreiber, Rachel Argaman, Anat Av-Gay, Yossef Nan, Helena M. Kattevilder, Alfred
                                                                                                                                                                                                                    ; Sequence 7, Application US/08386729A; Patent No. 5753435; GENERAL INFORMATION:
                                                                                                                              310 CMAALDAEHYLQEVGAQ 326
                                                                                                        295 SIAAQSAAEYIEHLNDQ 311
                                                                                                                                                                                                                                                                                                                                                                                                                      Pallissa, Harriet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 854-3713
FPORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 334 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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US-08-386-729A-7
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 DLMDNCRAQSVRFGTNILSETVTEVDFSARPFRVTSDSTTVLADTVVVATGAVARRLHFS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GEQELGGRGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 RAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTK-----DGSEETHEADGV 235
                                                                                                                                                                                              DRAFKNDKIDFIWSHTTKSINEKDGKVGSVT--LTSTKDGSEETHEADGVFIYIGMKPLT 245
                                                                                                                                                                                                                                                             246 APFKDLGITNDVGYIVTK----DDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300
                                                                                                                                                                                                                                                                                68 MFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQEL 127
                                                                                  128 GGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRILQ 187
           17 VIILGSGPAGYSAAVYAARANLKPLLITGMQAGGQLTTTTEVDNWPGDPHGLTGPALMQR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VCIIGSGPAAHTAAIYAARAELKPVLFEGWMANDIAAGGQLTTTTDVENFPGFPTGIMGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 IAIIGAGPAGMTAAVYASRANIKTVMIERGI-----PGGQMANTEEVENFPGFEM-ITGP
                                                                                                                                                                                                                       197 DKLQARVAEGKIVLKINAEVDEVLGDTMGVTGVRLKTRDGGSEEIAVDGMFVAIGHTPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
31.6%; Score 524.5; DB 4; Length
Best Local Similarity 39.1%; Pred. No. 4.2e-44;
Matches 124; Conservative 44; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09540014 Patent No. 6380372 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cho, Myeong-Je
Del Val, Greg
Caillau, Maxime
Lemauz, Peggy G.
Buchanan, Bob B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                     301 AAEYIEHL 308
                                                                                                                                                                                                                                                                                                                                                                    316 VERYLDSL 323
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APPLICANT:
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                                                           63 DLSTKMFEHAKKFGAVYQYGDIKSV-------EDKGEYKVINFGNKELTAKAV 108
                                                                       109 IIATGABYKKIGVPGEQELGGRGVSYCAVCDGA--FFKNKRLFVIGGGDSAVEFGTFTTK 166
                                                                                                         9 IAIIGAGPAGWTAAVYASRANLKTVMIERGI-----PGGQMANTEEVENFPGFEM-ITGP 62
                                      Best Local Similarity 37.5%; Pred. No. 5.4e-43;
Matches 121; Conservative 54; Mismatches 115; Indels 33; Gaps
                                                                                                                                                                                                  283 GLRQIVTATGDGSIAAQSAAEYI 305
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299 RYRQAITSAGSGCVAALEAEKFI 321
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Search completed: September 15, 2004, 12:22:10 Job time: 33 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 15, 2004, 12:05:48 ; Search time 125 Seconds (without alignments) 723.322 Million cell updates/sec

US-09-825-212-1 1662 1 MGTEIDFDIAIIGAGFAGMT......AAEYIEHLNDQARFHHHHH Title: Perfect score: Sequence:

Scoring table:

1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp200s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp203s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		ABB04148	AAITOO834	ARM722EO	ADARGSON	AAY29854	ABP60916	AAY29855	AAG82024	ARP60849	AA020618	ADDOKES	10000000000000000000000000000000000000	ABD60006	AD500000	ADD26570	ABF4066/	ABF60863	ABB49968	AUB00026	ABF268/9	ABB54256	ABF60904	ABP26878	ABP60919	ABU01907	ARDEORGA	2000
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325											80	00	28	28	· œ	00	. ~	326 5	
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26	28	53	30	31	32	33	34		36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

ABBO4148 XX AC ABB XX X
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'note= "Optional disulphide bond; formed when thioredoxin s reduced and broken when FAD is oxidised"
                                                                                                                                                                                                                                               315. .320 ---/note= "Histidine tag; aids the purification of the protein"
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                                                                                                                                                                                                                       .83. .289
[abel= NADPH_binding_site
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label= NADPH_binding_site
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label= NADPH_binding_site
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'label= NADPH_binding_site
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|label= NADPH_binding_site
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|abel= Nr<sup>-</sup>
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                                                                                                                                                           .260
label=
                                           148.
                                                                                                                                                                                                                                                    Misc-difference
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                       Disulfide-bond
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06-APR-2000; 2000US-0195055P.

(PHAA) PHARMACIA & UPJOHN CO

Benson TE;

WPI; 2002-034237/04.

Crystallizing Staphylococcus aureus thioredoxin reductase molecule or molecular complex by preparing purified thioredoxin reductase and crystallizing from solution comprising dimethyl sulfoxide and sodium formate.

Claim 52; Fig 11; 147pp; English.

The present sequence is that of a recombinant Staphylococcus aureus
thioredoxin reductase (TrxB) the crystal structure of which is solved in
thioredoxin reductase (TrxB) the crystal structure of which is solved in
the specification. Thioredoxin reductase is a two domain protein composed
to fa flavin adenine dinucleotide (FAD) binding domain and a reduced betanicotinamide adenine dinucleotide phosphate (NADPH) binding domain. The
specification describes the crystallisation of S. aureus thioredoxin
reductase molecule or molecular complex. The crystal of the invention may
be used to design an inhibitor of S. aureus thioredoxin reductase
cetuvity. The method is useful for crystallising a S. aureus thioredoxin
reductase molecule or molecular complex. The crystal obtained is useful
to roughing inhibitors of S. aureus thioredoxin reductase. A complexes and
designing inhibitors of S. aureus thioredoxin reductase. A composition
comprising the inhibitor is useful for preventing and treating S. aureus
thioredoxin reductase mediated disease

New isolated nucleic acid for use in diagnosing Staphylococcus infections and in vaccines for eliciting immune responses to the infections. ö 240 241 MKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS 300 180 Thioredoxin reductase; TrxB; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; neonatal conjunctivitis; osteomyelitis; skin infection; scalded skin syndrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis. RAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIG 181 KAQKILQDRAFKUDKIDFIWSHTIKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIXIG GPDLSTKMPEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDEL 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMIT Gaps 0 Length 320; Indels DB 5; o; Score 1662; DB 5. Pred. No. 3e-146; Mismatches 192. .194
/label= Antigenic_epitope
210. .212 /label= Antigenic_epitope S. aureus thioredoxin reductase, TrxB Location/Qualifiers Ž AAEYIEHLNDQARSHHHHHH 320 AAEYIEHLNDQARSHHHHHH 320 AAU00834 standard; protein; 312 100.0%; Sc 100.0%; Pr ive 0; 99US-0151933P (HUMA-) HUMAN GENOME SCI INC. 31-AUG-2000; 2000WO-US023773 (first entry) Best Local Similarity 100. Matches 320; Conservative Staphylococcus aureus. WPI; 2001-183259/18. N-PSDB; AAS00915. Similarity Sequence 320 AA; WO200116292-A2 01-SEP-1999; 04-JUL-2001 241 AAU00834; Choi GH; 181 301 301 61 121 61 Query Match Region Region AAU00834 g ð 셤 à X S qq ò ď à g ò

us-09-825-212-1.rag

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Staphylococcus infections. The polypeptides of the invention are used to detect anti-Staphylococcus antibodies in a biological sample from an ential to diagnose Staphylococcus infections. The polypeptides are also used in vaccines to elicit protective antibodies in an animal to a member of the Staphylococcus genus and for preventing or attenuating an infection caused by a member of the Staphylococcus genus e.g wound infection, callulitis, burn infection, evelid infection, food poisoning, collection, and an accompanies, skin infection, disease and Lypall's disease, toxic spock syndrome and endocarditis. The polymucleotides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides on vivo diagnostic and therapeutic methods
                                       The sequence represents S. aureus TrxB (Thioredoxin reductase). The polymucleotides of the invention are used to detect Staphylococcus nucleic acids in a biological sample from an animal for diagnosing
                                                                                                                                                                                                                                                                                                                                       Length 312;
                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGT
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                                                                                                                                                                                                                                                                                                                                  Score 1593; DB 4;
Pred. No. 7.7e-140;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus protein #1490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM72250 standard; protein; 311 AA
                 9; Page 16; 225pp; English
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                                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 99.4%;
Matches 310; Conservative
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                                                                                                                                                                                                                                                                                                   Sequence 312 AA;
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Sequence 311 AA;
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                                                                                    GPDLSTRWFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIG 120
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                                    MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIFGGQMANTEEVENFPGFEMIT
               MGTEIDFDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMIT
                                                                                                                     FADKVTIVHRRDEL
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                                                                                                                                                                                    RAQRILQDRAFKNDKIDFIWSHTLKSTNEKDGKVGSVTLTSTKDGSEETHEADGVFIYIG
                                                                                                                                                                                                                              MTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target;
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus
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27-MAR-2002; 2002WO-1B002637.

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The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                              protein, useful as a vaccine for treating or infection, specifically an infection caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLSTKWFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism; antibacterial; neuroprotective; immunosuppressive; antiinflammatory; antiulcer; immunostimulant; ophthalmological; pathogenic microbe; bacteraemia; septic shock; organ infection; skin infection; bacterial basal colonisation; bacterial eye infection; septicaemia; tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1582; DB 6;
Pred. No. 8.1e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus antigenic protein #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2980; 49pp; English.
                                                                          Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA89500 standard; protein; 309 AA.
     27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.2%;
                                                                                                                                                         New Staphylococcus aureus
                                                                                                                                                                               preventing Staphylococcal
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Best Local Similarity 99.4<sup>1</sup>
Matches 308; Conservative
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                                                                                                        WPI; 2003-120786/11.
                                  (CHIR-) CHIRON SPA
                                                                                                                            N-PSDB; ACF73810
                                                                     Masignani V,
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242 181

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an antigenic protein or its part, which is for use as a vaccine. The antigenic protein is encoded by an isolated is for use as a vaccine. The antigenic protein is encoded by an isolated by a molecule of Staphylococcus aureus or S. epidermidis partial gene sequences (designated dnash and dna SE, respectively; and which encodes a protein expressed by a pathogenic organism. Also described: (1) a vaccine composition comprising at least one antigenic protein; (2) a method of composition animal against a disease or condition caused by a pathogenic microbe by administering the antigenic protein or the vaccine; pathogenic microbe by administering the antigenic protein or the vaccine; (3) an antibody or its binding part obtainable by the method above; (4) composition antigens call line produced by the method of (4); and (6) identifying openic antigens have antibacterial, neuroprotective, immunosuppressive, antiinflammatory, antiulcer, immunostimulant and ophthalmological cutivities, and can be used in vaccines. The antigenic proteins or activities, and can be used in vaccines. The antigenic proteins or activities, and can be used for immunising an animal (specifically a human) against a disease or condition caused by a pathogenic microbe, e.g. capainst a disease or condition caused by a pathogenic microbe, e.g. capainst a colonisation, bacterial eye infections, septicaemia, tuberculosis, bacterial eye infections, septicaemia, tuberculosis, capacteria-associated food poisoning, blood infections, peritonitis, encodition, imperigo, histoplasmosis, lyme disease, gastro-enteritis, dysentery, shigellosis, S. aureus-associated septicemial, peritonitis or sationary and antiparic antiparic processed antiparic processed antiparic expressed septicaemia, peritonitis or sationary and antiparic antiparic antiparic antiparic antiparicaemia, peritonitis antiparic antiparic antiparicaemia, peritonidis-antiparicaemia, peritonidis-antiparicaemia, peritonidis-antiparicaemia, peritonidis-antiparicaemia, perit
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                                                                                                                                                                                                                                                                                                                                                                                              New antigenic polypeptides from Staphylococcus aureus or S. epidermidis, useful as a vaccine for immunizing humans against e.g. bacteremia, septic shock, septicemia, tuberculosis, meningitis, pneumonia, gonorrhea or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock; necrotising fasciitis; impetigo; histoplasmosis; Lyme disease; gastro-enteritis; dysentery; shigellosis; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocarditis. The present sequence represents a S. aureus antigenic protein sequence from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 131; 189pp; English.
                                                                                                                                                                                                                                                                                                                                    Clarke S,
                                                                                                                                                                                        02-AUG-2002; 2002WO-GB003606
                                                                                                                                                                                                                            02-AUG-2001; 2001GB-00018825
09-JAN-2002; 2002GB-00000349
                                                                                                                                                                                                                                                                                 (UYSH-) UNIV SHEFFIELD. (BIOS-) BIOSYNEXUS INC.
                                                                                 Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                      Mond J,
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Best Local S:
Matches 306
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182
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                                       242
                                                                                                               302
                                                                                                                                   242 PLIAPFKDLGIINDVGXIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents Staphylococcus thioredoxin reductase (TrxB). TrxB inhibitors can be used as antimicrobials to treat a Staphylococcus, particularly S. aureus, infection. TrxB inhibitors are antimicrobials to which, unlike most of those in the prior art, Staphylococcus has not yet developed a resistance
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122 GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFLTKFADKVTIVHRRDELRA
                                     QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK
                                                           PLTAPFYDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus trxB open reading frame protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus; trxB; thioredoxin reductase; antimicrobial.
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ilarity 98.1%; Pred. No. 7.4e-137;
Conservative 1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus
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Multimeric protein; redox protein; thioredoxin; thioredoxin reductase; oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic; vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer; food product; milk; wheat; oxidative stress; cateract; diabetes; chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis; bronchiopulmonary disease; malignancy; reperfusion injury; wound healing; gastro intestinal bleeding; intestinal bowel disease; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing oil body associated with recombinant multimeric protein compley. redox proteins and immunoglobulins comprises producing recombinant polypeptides capable of forming the complex in cells comprising oil
                                 PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dalmia BK;
                                                                                                                                                                                                                             Staphylococcus aureus thioredoxin reductase SEQ ID NO:265.
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Moloney M;
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                                                                                                                                                        ABP60916 standard; protein; 311 AA.
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                  disease
                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2000; 2000US-00742900.
05-JUL-2001; 2001US-0302885P.
04-DEC-2001; 2001US-00006038.
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                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                gastro oesophageal reflux
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Zaplachinski
                                                                              EYIEHLNDQA 312
                                                                                                   GYIEHLNDOA 311
                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
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        and ABP60677 to
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                                                                                                                                                                                                                   GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                      PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                                                                                                                              62
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(gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 t
ABP60964 represent sequence given in the exemplification of the present
                                                                                                                     3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                                                                                                            2 TEIDFDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                                                                                                                                                                                                                                  QRILODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK
                                                                                                                                                                                                                                                                                  The present sequence represents Staphylococcus thioredoxin reductase (TrxB). TrxB inhibitors can be used as antimicrobials to treat a Staphylococcus, particularly S. aureus, infection. TrxB inhibitors are antimicrobials to which, unlike most of those in the prior art, Staphylococcus has not yet developed a resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis trxB open reading frame protein sequence.
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                                                                             Length 311;
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                                                                           Score 1561; DB 5;
Pred. No. 7.4e-137;
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                                                                                                 Mismatches
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                                                                         93.9%;
98.1%;
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                                                                                     Local Similarity
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                                                Sequence 311 AA;
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                                                                                               Matches 304;
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The present invention describes a method (M1) for producing an oil body associated with a recombinant multimeric protein complex (MPC). MI comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (PL, P2), where P1 is capable of associating with CC P2 to form the MPC and associating the complex with an occlusion body CC P1. M1 is useful for producing an oil body associating with OB and CC P1. M1 is useful for producing an oil body associated with a recombinant CC MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care CC product which reduces the oxidative stress on the surface area of the chuman body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis, cataracts, cmalignancies, reperfusion injury, wound healing, sepsis, gastro CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD

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19-DEC-2001; 2001WO-US050240.
                                                                                                                                        Sequence 310 AA;
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06-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (II), given in AAG81454 to AAG83120, from Stabhylococcus epidermidis. (I) and have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the
                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
                                                                                                                                                                                                                    PLIAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
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                                                                3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPGFEMITGP
                                                                                                     DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP
                                                                                                               GEQELGGRGVSYCAVCDGAFFRNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA
                                                                                                                                                                                QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLISTKDGSEETHBADGVFIYIGMK
                                                                               TEVDFDVAIIGAGPAGATAAVYASRANLKTVMIERGAPGGQMANTEEVENFPGFEMITGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                    S. epidermidis open reading frame protein sequence SEQ ID NO:1142.
                                                .
0
                             Length 310;
                                               Indels
                                                  13;
                           Match 87.5%; Score 1455; DB 2; Local Similarity 90.3%; Pred. No. 5.6e-127; Les 278; Conservative 17; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 330; 2188pp; English.
                                                                                                                                                                                                                                                                                                                               AAG82024 standard; protein; 310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-2000; 2000WO-US030782
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N-PSDB; AAH52874.
            Sequence 310 AA;
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polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polymucleotide sequences from the present invention. AAH55091 to AAH55099 represent oligomucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polymucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLSTKWFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 1455; DB 4; Length 3; Pred. No. 5.6e-127; 17; Mismatches 13; Indels
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Best Local Similarity 90.31
Matches 278; Conservative
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The present invention describes a method (MI) for producing an oil body associated with a recombinant multimeric protein complex (MPC). MI comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (PI, P2), where PI is capable of associating with CP2 to form the MPC and associating the complex with an occlusion body CP3 to form the MPC and associating the complex with an occlusion body CP1 MI is useful for producing a noil body associating with OB and MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care burman body or used to lighten the skin, or a pharmaceutical composition used to reat chronic obstructive pulmonary disease (COPD), cataracts, disbetes, envenomation, bronchiopulmonary disease, psoriasis, and intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD context and a composition of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing oil body associated with recombinant multimeric protein comple
e.g. redox proteins and immunoglobulins comprises producing recombinant
polypeptides capable of forming the complex in cells comprising oil
                                                                                                                                                                                                                                                                               Heifetz PB,
Moloney M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 82; Page 268-269; 362pp; English.
                                                                                                                                                                       (SEMB-) SEMBIOSYS GENETICS INC. (SYGN ) SYNGENTA PARTICIPATIONS AG
                                         19-DEC-2000; 2000US-00742900.
05-JUL-2001; 2001US-0302885P.
04-DEC-2001; 2001US-00006038.
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Val G, Zaplachinski
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                                      19-DEC-2000;
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Length 315; 55; Indels 69.4%; Score 1154; DB 5; 71.4%; Pred. No. 6.5e-99; ; Pred. No. 6.5e 33; Mismatches Matches 220; Conservative 307 HLNDQARS 314 Local Similarity 246 99 187 Query Match 67 g ò g à à g g à 셤 à à

126 125 186 QDRAFKNDKIDFIWSHTIKSINEKDGKVGSVTLISTKDGSEETHEADGVFIYIGMKPLTA 246 186 QARAFDNEKVDFLMNKTVKEIHEENGKVGNVTLVDTVTGEESEFKTDGVFIYIGMLPLSK 245 247 PFKDLGITNDVGYIVTKDDMTTSVPGIPAAGDVRDKGIRQIVTATGDGGIAAQSAAEYIE 306 99 65 7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST YOVIIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGGMANTEDVENYPGFESILGPELSN KMFEHAKKPGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIGVPGEKE 127 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE Gaps 0; ELQETLKT 313

AAO20618 standard; protein; 315 AA.

RESULT 10 AAO20618 ID AAO2

AAO20618;

(first entry) 10-APR-2003

Thioredoxin reductase variant protein sequence #17.

Ophthalmological; virucide; vulnerary; vasotropic; antiallergic; cofactor specificity; thioredoxin reductase; TR; non-allergenic food; computational mutagenesis; scaffold protein; oil body; animal feed; digestibility; gluten; protein disulfide isomerase; PD; enzyme; scleroprotein; gelled; food; nitrosative stress response; eye disease; cataract; oxidative stress; ischemic-reperfusion; acute lung injury.

Bacillus subtilis.

complex

Dalmia BK;

Briggs SP,

WO200290300-A2

14-NOV-2002

06-MAY-2002; 2002WO-US01435B.

04-MAY-2001; 2001US-0289029P

05-APR-2002; 2002US-0370609P. 29-APR-2002; 2002US-00370609.

XENCOR (XENC-)

SYGN) SYNGENTA PARTICIPATIONS AG.

Desjarlais JR, Heifetz Del Val G, P, Muchhal U; Dalmia BK, Briggs SP, Luginbuhl E

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WPI; 2003-111951/10.

Altering cofactor specificity of target protein, e.g. thioredoxin reductase, useful for reducing antigenicity of glutens in wheat, barley, or treating disulfide linkages present in proteins, by computational mutagenesis

Disclosure; Fig 21B; 212pp; English.

The invention retarget to a novel method for attering the cofactor operations to a target protein (e.g. thioredoxin reductase (TR)) by computational mutagenesis. This method involves inputting a set of condinates for a scaffold protein comprising amino acid positions, applying at least one protein design cycle; and generating a set of candidate variant proteins with altered cofactor specificity. The novel proteins chosen from Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces, Neurospora crassa, Arabidopsis, and human. Another compared to interpretation of non-altergenic foods, or in the preparation of non-altergenic foods, or in the preparation of animal feeds to improve the digestibility of the feeds. The variant TR protein is useful for reducing the antigenicity of glutens in wheat, rye or barley, to reduce alternative substrates for thioredoxin reductases, including a number of plant and mammalian proteins found to contain the protein su useful as a redox partner in compositions used for treating corpositions comprising variant TR proteins such as scleroproteins. Compositions comprising variant TR proteins and PDI are useful for method of the inventions; and thus is useful in food processing a further compositions comprising variant TR proteins and PDI are useful for method of the invention is useful in food processing. A further method of the invention is useful in food processing a further compositions, and thus is useful in food processing or animal dispersently composition in useful in sprotein quality as well as grains that perform qualitatively differently variant TR protein quality as well as grains that perform quality in the protein quality is a variant provented or an invention in useful perform quality in the protein quality as well as grains that perform quality in the protein quality as well as grains that perform quality in the protein quality as well as grains that perform quality in the protein in the protein in the protein in the protein in the protein in the protein i variant TR proceins in combination with thioredoxin, which can used to manipulate nitrosative stress, to upregulate nitrosative stress responses, and thus is useful for treating eye diseases, such as catearacts, where it inhibits or reverse formation of cataract in eye. The variant TR protein in combination with thioredoxin is also useful for minimizing oxidative stress and ischemic-reperfusion induced in acute invention relates to a novel method for altering the cofactor

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186
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                                                                                                                                                               QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                                                                                                                                                                                       9
                                                                                                                                                                         7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
                                                                               KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE
                                                                                                                  66 KMFEHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIGVPGEKE
                                                                                                                                 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL
                                                                                                                                          lung injury. This sequence represents a thioredoxin reductase variant protein of the invention
                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                            Thioredoxin reductase; TRR; cofactor specificity; computational mutagenesis; substrate specificity; PDA; protein design automation; toxic protein; food allergenicity; food digestibility.
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                                         Length 315;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desjarlais JR,
                                          69.4%; Score 1154; DB 6; 71.4%; Pred. No. 6.5e-99;
                                                         33; Mismatches
                                                                                                                                                                                                                                                                                   ADD26553 standard; protein; 315 AA.
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05-APR-2002; 2002US-0370609P.
29-APR-2002; 2002US-0376682P.
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                                                                                                                                                                                                                                                                                                                  15-JAN-2004 (first entry)
                                           Query Match
Best Local Similarity 71.4%
Matches 220; Conservative
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HEIFETZ P.
LUGINBUHL P.
                                                                                                                                                                                                                               307 HLNDQARS 314
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BRIGGS S P.
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                             Sequence 315 AA;
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The invention relates to altering the cofactor specificity of thioredoxin careductase (TRR) comprising computational mutagenesis. Also included are reductase (TRR) comprising computational mutagenesis. Also included are carget protein, a variant TRR protein that reduces a protein that reduces a thioredoxin protein (obtained from an organism selected from a thioredoxin protein (that is either a wild-type TRR protein fused.) Neurospora crassa, Arabidopsis, and human), a variant TRR protein fused to a second protein (that is either a wild-type TRR protein, thioredoxin, or a variant TRR protein), producing a plant with a modified TRR protein, or a variant TRR protein (the cofactor specificity of the variant TRR is altered transformed plant. The cofactor specificity of the variant TRR is altered to that the variant preferentially binds NADPH compared to NADH, or such that the variant preferentially binds NADPH compared to NADH, or such that the variant preferentially binds NADPH compared to the corporate field calculation. The variant TRR protein last gornthum, or a force field calculation. The variant TRR protein has 1.3 amino caid substitutions are selected from positions A4, A5 and A6, the amino acid substitutions are selected from positions A4, A5 and A6, preferably from RA4W, RA5L, RA5M, RA5I, RA5F, RA5V, RA5Y, RA5T, RA6B, CC RA6C, RA6C, AR6W, RASI, RASH, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RASI, RA
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Altering the cofactor specificity of thioredoxin reductase, useful for reducing the toxicity of toxic proteins, reducing allergenicity of food and increasing the digestibility of foods, comprises computational
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                                                                                                                                                                                                                 Disclosure; Fig 21; 125pp; English
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Best Local Similarity 71.4<sup>1</sup>
Matches 220; Conservative
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                                                                                                                                             mutagenesis.
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cofactor specificity; thioredoxin reductase; TR; non-allergenic food; computational mutagenesis; scaffold protein; oil body; animal feed; digestibility; gluten; protein disulfide isomerase; pTI; enzyme; scleroprotein; gelled; food; nitrosative stress response; eye disease; cataract; oxidative stress; isohemic-reperfusion; acute lung injury. vulnerary; vasotropic; antiallergic; virucide; Ophthalmological;

Unidentified

WO200290300-A2

14-NOV-2002

06-MAY-2002; 2002WO-US014358

04-MAY-2001; 2001US-0289029P. 05-APR-2002; 2002US-0370609P. 29-APR-2002; 2002US-00370609.

(XENC-) XENCOR

(SYGN) SYNGENTA PARTICIPATIONS AG.

Heifetz P; Desjarlais JR, ტ Val Del Muchhal U; Dalmia Luginbuhl P, Briggs SP,

WPI; 2003-111951/10

barley, Altering cofactor specificity of target protein, e.g. thioredoxin reductase, useful for reducing antigenicity of glutens in wheat, bar] or treating disulfide linkages present in proteins, by computational

Disclosure; Fig 22; 212pp; English.

The invention relates to a novel method for altering the cofactor of specificity of a target protein (e.g. thioredoxin reductase (TR)) by computational mutagenesis. This method involves inputting a set of coordinates for a scaffold protein comprising amino acid positions, coordinates for a scaffold protein comprising amino acid positions, condidate variant proteins with altered cofactor specificity. The novel candidate variant proteins with altered cofactor specificity. The novel proteins chosen from Escherichia coli, Bacillus subtilis, Mycobacterium controlis useful for altering the cofactor specificity. The novel legrate, Saccharomyces, Neurospora crassa, Arabidopsis, and human. Another controlis useful for making oil bodies which are useful canimal feeds to improve the digestibility of the feeds The variant TR protein is useful for reducing the antigenicity of glutens in wheat, rye including a number of plant and mammalian proteins found to contain the preparation of manims e.g. protein disulfide isomerase (PDI). The variant TR protein is useful as a redox partner in compositions useful for contain and summalian proteins compositions compassing a redox partner in compositions useful for contain compositions compassing variant TR proteins such as enzymes, e.g., proteases, compositions compassing variant TR proteins manylages tet; and structural proteins such as enzymes, e.g., proteases, compositions, and thus is useful for producing plants expressing variant TR protein, e.g., corn and soybean provides grains with altered storage protein quality as well as grains that perform qualitatively differently form ormal grain during industrial processing or animal digestion of manipulate nitrosative stress, and thus is useful for treating proteins in combination with thioredoxin, which can used to manipulate nitrosative stress, and thus is useful for treating or animal different in combination with thioredoxin, where it inhibits or reverse formation every and every and every and industing any and indused in acute of w This sequence represents a thioredoxin reductase variant lung injury. This sequend protein of the invention

Sequence 315 AA;

Query Match

6; Length 315; DB Score 1152; 69.3%;

ö 126 KMFEHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIGVPGEKE 125 127 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186 LGGRGVSYCAVCDGAFFKGKELVVVGGGDSAVEEGVYLTRFASKVTIVHRRDKLRAQSIL 185 QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246 306 99 65 KWFBHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE 7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST 6 YDVIIIGAGPAGMTAAVYTSRANLSTLMIERGIPGGQMANTEDVENYPGFESILGPELSN PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE Gaps . Indels 55; le-98; Mismatches Pred. No. 34; 71.18; Conservative 306 ELQETLKT 313 307 HLNDQARS 314 Best Local Similarity 219; 67 126 187 247 Matches 셤 à g ò 9 ð dd ð g à q

RESULT 13

ABP60886 standard; protein; 315 AA **AB**P60886

ABP60886;

(first entry) 06-SEP-2002

Bacillus halodurans thioredoxin reductase SEQ ID NO:235.

Multimeric protein; redox protein; thioredoxin; thioredoxin reductase; oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic; vasorropic; vulnerary; antibacterial; immunosuppressive, antilulcer; food product; milk; wheat; oxidative stress; cataract; diabetes; chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis; bronchiopulmonary disease; malignancy; reperfusion injury; wound healing; gastro intestinal bleeding; intestinal bowel disease; ulcer;

Bacillus halodurans

WO200250289-A1.

27-JUN-2002

19-DEC-2001; 2001WO-US050240.

19-DEC-2000; 2000US-00742900. 05-JUL-2001; 2001US-0302885P. 04-DEC-2001; 2001US-00006038.

SYGN) SYNGENTA PARTICIPATIONS AG SEMB-) SEMBIOSYS GENETICS

Briggs SP, Dalmia BK; Heifetz PB, Moloney M; Van Rooijen G, Deckers H, Del Val G, Zaplachinski S,

WPI; 2002-508806/54.

Producing oil body associated with recombinant multimeric protein complex e.g. redox proteins and immunoglobulins comprises producing recombinant polypeptides capable of forming the complex in cells comprising oil

Claim 82; Page 296-297; 362pp; English.

06-MAY-2002; 2002US-00141531

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The present invention describes a method (MI) for producing an oil body associated with a recombinant multimeric protein complex (MPC). MI comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (PI, P2), where P1 is capable of associating with CC recombinant polypeptide (PI, P2), where P1 is capable of associating with CC P2 to form the MPC and associating the complex with an occlusion body CC (OB) through an OB-targeting-protein capable of associating with OB and CC P1. MI is useful for producing an oil body associated with a recombinant CC a food product such as milk or wheat based food product, personal care to man a milk or wheat based food product, personal care common to be stress on the sufface area of the product which reduces the oxidative stress on the sufface area of the chuman body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, envenomation, bronchiopulmonary disease (COPD), cataracts, calabetes, envenomation, bronchiopulmonary disease (BDD), ulcers, GERD intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (ST to ABP60664 represent sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 TGPDLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LGPELSTKMFEHAKKFGAEYAYGDIKEIIDQGDLKLVKAGNKEYKARAVIVATGAEYKKL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 GMKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thioredoxin reductase; TRR; cofactor specificity; computational mutagenesis; substrate specificity; PDA; protein design automation; toxic protein; food allergenicity; food digestibility; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                            68.9%; Score 1145.5; DB 68.6%; Pred. No. 4.1e-98; tive 38; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B. subtilis synthetic thioredoxin reductase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.9%
Best Local Similarity 68.6%
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 315 AA;
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The invention relates to altering the cofactor specificity of thioredoxin concuctase (TRR) comprising computational mutagenesis. Also included are reductase protein, a variant TRR protein that reduces a protein that reduces a thioredoxin protein (obtained from an organism selected from a thioredoxin protein (obtained from an organism selected from Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharcmyces, CC assord protein (that is either a wild-type TRR protein, thioredoxin, or a variant TRR protein), producing a plant with a modified TRR protein, therefore a transformed plant. The offactor specificity of the variant TRR is altered contransformed plant. The offactor specificity of the variant TRR is altered such that the variant preferentially binds NADPH compared to NADH, or vice versa. The protein design cycle comprises protein design algorithm, or a force field calculation. The variant TRR protein also the constitutions as compared to the wild-type Arabidopsis TR protein. The variant TRR protein has 1-3 amino caid substitutions as compared to the wild-type Arabidopsis TR protein. The variant preferably from RA4W, RA51, RA5M, RA51, RA51, RA57, RA57, RA69, RA60, and RA6N. The method is useful for reducing the toxicity of toxic proteins, reducing allergenicity of food and increasing the coxicity of toxic proteins, reducing allergenicity of food and increasing the coxicity of the method as compared to prior art. The present sequence is a synthetic contractional fragments of a wild-type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 KMFEHAKKFGAEYAYGDIKEVIDGKEYKVVKAGSKEYKARAVIIAAGAEYKKIGVPGEKE 125
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                                                                                                                                                                                                                                                                                                                                       for
food
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                                                                                                                                                                                                                                                                                                                                    Altering the cofactor specificity of thioredoxin reductase, useful reducing the toxicity of toxic proteins, reducing allergenicity of and increasing the digestibility of foods, comprises computational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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69.5%; Pred. No. 5.9e-93;
ive 33; Mismatches 55; Indels (
                                                                                                                                                                                                                                                    Heifetz
                                                                                                                                                                                                                                                  Desjarlais JR,
                                                                                                                                                                                                                                                      Val GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 30; Page; 125pp; English.
                              04-MAY-2001; 2001US-0289029P.
05-APR-2002; 2002US-0370609P.
29-APR-2002; 2002US-0376682P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.6
Best Local Similarity 69.5
Matches 214; Conservative
                                                                                                                                                                                                                                                          Dalmia BK, Briggs SP, Tuginbuhl P, Muchhal U;
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HEIFETZ P.
LUGINBUHL P.
                                                                                                                                                                                                                                                      Briggs SP,
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BRIGGS S P.
VAL G D.
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Gaps 1;

Length 315;

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Bacillus subtilis. US2003100743-A1.

Synthetic

29-MAY-2003

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us-09-825-212-1.rag

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PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAABYIE 306
                ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP33124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can particularly S. epidermidis infections. The sequences can be used to secree for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                        Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                            Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.2%; Score 1083; DB 5; Length 2: Best Local Similarity 85.7%; Pred. No. 2e-92; Matches 209; Conservative 14; Mismatches 21; Indels
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                                                                                                                                                         ABP40667 standard; protein; 253 AA.
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97US-0064964P.
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N-PSDB; ABN93212.
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08-NOV-1997;
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LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186 QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246

KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE

67 6 127 69 187

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68

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129 QERAFKNDKVDFIWSHTLKTINEKDGKVGSVTLESTKDGAEQTYDADGVFIYIGMKPLTA 188
                        247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEXIE 306
                                        307 HLND 310
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Search completed: September 15, 2004, 12:18:46 Job time : 128 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

September 15, 2004, 12:13:58; Search time 40 Seconds (without alignments) 769.532 Million cell updates/sec Run on:

US-09-825-212-1

Perfect score: Sequence: Title:

1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHHH Scoring table:

320

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
1: pir3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 B89849 C198616: Staphylococcus aureus C19Accession: E89849 C19Accession: E89849 R14. Wizutani-U1, Y.; Kobayasi C1, Shiba, T.; Hattori, M.; Ogalance 37, 1225-1240, 2001 A,Title: Whole genome sequencing A,Title: Whole genome	RESULT 1 B89849 Libroredoxine reductase [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Accession: B89849 C;Accession: B89849 R;Auroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc R;Xuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc R;Xuroda, M.; Ohta, T.; Hattori, M.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Scatus: preliminary A;Molecule type: DNA A;Residues: 1311 < kUR, A;Residues: 1311 < kUR, A;Residues: 1311 < kUR, A;Residues: 1311 < kUR, A;Resperimental source: strain N315 C;Genetics: C;Genetics: A;Genetics:
Query Match Best Local Similarity Matches 308; Conserva	cch 11 Similarity 99.4%; Pred. No. 2.9e-111; 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 3 TEI Db 2 TEI	TEIDFDIAIIGAGPAGMTAAVYASRANLKITVMIERGIPGGQMANTEEVENFPGFEMITGP 62
Qy 63 DLS bb 62 DLS	DLSTKMFEHAKKEGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEVKKIGVP 122
Qy 123 GEQ Db 122 GEQI	GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
OY 183 ORII Db 182 ORII	QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
Qy 243 PLT3 Db 242 PLT3	PLTAPEKDLGITUDVGYIVTKDDMITSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
Oy 303 EYII Db 302 EYII	EXIEHINDA 312

RESULT

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C;Accession: C84096
C;Accession: C84096
Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
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                                                                                                                           C;Species: Bacillus subtilis
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
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                                                                thioredoxin-disulfide reductase (EC 1.8.1.9) - Bacillus subtilis
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C. Accession: D86742
R. Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001
A.; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s. A.; Reference number: A86625; MuID:21235186; PMID:11337471
A.; Accession: D86742
A.; Accession: D86742
A.; Accession: D86742
A.; Molecule type: DNA
A.; Residues: 1-308 < STO>
A.; Cross-references: GB:AE005176; PID:g12723876; PIDN:AAK05038.1; GSPDB:GN00146
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                                                                                                                                                                   thioredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Lactococcus lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GROELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEIIQQRAFKEEKINFIWDSVPMEIKGDDKKVQSVVYKNVKTGEVTEKAFGGIFIYVGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.5%; Score 872; DB 2; 53.1%; Pred. No. 5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain IL1403
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KFVAELD 308
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-303 < KUR>
                                            ELKE 311
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les 163;
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Best Local S:
Matches 163
                                            308
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Liboredoxin reductase [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001
C;Accession: AF1384
C;Accession: AF1384
C;Accession: AF1384
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C;Accession: AF1384
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C;Accession: AF1384
D; Jones, L.M.; Karst, U.
Science 294, 849-882, 2001
A;Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Residues: 1-319 <GLA>
A;Residues: 1-319 <GLA>
A;Residues: 1-319 <GLA>
A;Residues: 1-319 <GLA>
A;Cross-references: GB:MC 003210; PIDN:CAD00556.1; PID:gl6411966; GSPDB:GN00177
C;Genetics:
A;Gene: trxB
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
                                                                            KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE 126
                                                                                                              LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
                                                                                                                                                                                                                QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                                                                                                                                                                                                                                                                                                 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
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7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
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65.5%; Pred. No. 1.2e-71;
ive 43; Mismatches 62;
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T.; Zalewski, C.; Ma
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A,Status: proliminary
A,Molecule type: DNA
A,Residues: 1-325 cWHI>
A,Escidues: 1-325 cWHI>
A,Escidues: 1-325 cWHI>
A,Escidues: 1-325 cWHI>
A,Escidues: 1-325 cWHI>
A,Cross-references: GB.AE002036; GB.AE000513; NID:g6459766; PIDN:AAF11534.1; PID:g645977
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Deinococcus radiodurans (strain R1)
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
Cispecies: M. Species: M. Species: M. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. Sisen, J. 
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247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEXI- 305
                                                                                                                                                     241 FVKELNIQDQAGWIVTDNHMKTAVDGIFAVGDVRLKDLRQVTAVGDGALAGQBAYKFIT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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Eur. J. Blochem. 217, 791-798, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DELRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPGF-EMITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 PDLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFG----NKELTAKAVIIATGAEYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: DR1982
A;Map position: 1
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.8%; Score 728.5; DB 2;
48.4%; Pred. No. 3.1e-47;
tive 51; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A----QSAAEYIE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AMMTEROLAALEVE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.4
Matches 152; Conservative
                                                                                                                                                                                                                                                                           EH 307
                                                                                                                                                                                                                                                                                                                                                    EH 302
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C)Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: 035169
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.X.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Recence number: A95000; MUID:21357209; PMID:11463916
A;Recence number: A95000; MUID:21357209; PMID:11463916
A;Residues: 1-303 <br/>A;Residues: 1-304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ODRAFANEKISFIWDSVVKEI-KGENRVESVVFENVKTGQVTEQAFGGVFIYVGLDPLSD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYI- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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KMFEPLENLGVEHIXGYVENVEDHGDFKKVMTDDQTYETRTVIVATGSKHRPLGVPGEEE
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                                                                                                                                                                                                                                                                                                                             7 FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPGFEMITGPDLST
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A;Gene: SP1458
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
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                                      A,Gene: trxB
C,Superfamily: thioredoxin reductase, thioredoxin reductase homology
C,Keywords: oxidoreductase
                                                                                                                                                                    Query Match
51.2%; Score 851; DB 2; Length 303;
Best Local Similarity 54.0%; Pred. No. 1.9e-56;
Matches 163; Conservative 55; Mismatches 82; Indels
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Best Local Similarity 53.6%; Pred. No. 2.6e-56;
Matches 162; Conservative 57; Mismatches 81; Indels
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Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
                                          A, Reference number: S63987; MUID:96096738; PMID:8529640
                                                                                                                                                             A;Cross-references: EMBL:U24268; NID:g1171124
C;Genetics:
A;Gene: trxB
A;Start codon: GTG
C;Complex: homodimer; each chain has a tightly
C;Function:
                                                                                                       A; Molecule type: DNA
A; Residues: 1-117 < KRW>
                                                                                 Accession: S63989
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A; Reference number: S38988; MUID:9403119; PMID:8223622
A; Reference number: S38988; MUID:9403119; PMID:8223622
A; Residues: S38988; MUID:9403119; PMID:8223622
A; Molecule type: DNA
A; Residues: 1-315 c_LUEs
A; Cross-references: GB:L04500; NID:g2708733
B; Dietrichs, D: Meyer, M.; Schmidt, B.; Andreesen, J.R.
J. Bacteriol. 1122, 2088-2095, 1990
A; Reference number: A35156; MUID:90202731; PMID:2318809
A; Reference number: A35156; MUID:90202731; PMID:2318809
A; Reference number: A35156; MUID:90202731; PMID:2318809
A; Reference number: A35156; MUID:90202731; PMID:2318809
A; Reference number: A35156; MUID:90202731; PMID:2318809
A; Reference number: A35156; MUID:90202731; PMID:2318809
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A; Reference number: A35156; MUID:90202731; PMID:2318809
A; Reference number: A35156; MUID:90202731; PMID:2318809
A; Residues: 1-33, 'x', 35-46, 'x', 48, 'D', 50-55 cDIE>
C; Genetics:
A; Genetics:
A; Genetics:
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Eur. J. Blochem. 234, 192-199, 1995
A;Title: Glycine reductase of Clostridium litorale. Cloning, sequencing, and molecular
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A,Residues: 1-315 «KRB»
A;Cross-references: EMBL:U24268; NID:g1171124; PIDN:AAC43575.1; PID:g1171125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 FDIALIGAGPAGWTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPG-FEMITGPDLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQDRAFKNDKIDFIWSHTTKSINEKDGKVGS-----VTLTSTKDGSEETHEADGVFIYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.7%; Score 726; DB 1;
49.8%; Pred. No. 4.6e-47;
tive 50; Mismatches 96;
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**Kreimer, S.; Andreesen, J.R.

**Submitted to the EMBL Data Library, April 1995

**A.Reference number: 863990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.8
Matches 153; Conservative
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A; Description: catalyzes the reversible reduction of oxidized thioredoxin by NaDPH C; Superfamily: thioredoxin reductase, thioredoxin reductase homology C; Superfamily: thioredoxin reductase, thioredoxin reductase, radox-active disulfide F;1-309/Domain: thioredoxin reductase homology (F;1-309/Domain: thioredoxin reductase homology (F;1-309/Domain: thioredoxin reductase homology (F;1-309/Domain: thioredoxin reductase homology (F;1-309/Domain: beta-alpha-beta FAD nucleotide-binding fold F;134-137/Disulfide bonds: redox-active #status predicted
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A;Residues: 1-307 <COL>
A;Cross-references: GB:AE001252; GB:AE000520; NID:g3323119; PIDN:AAC65780.1; PID:g332312
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; they, L.; Weindman, J.; Smith, H.O.; Venter, J.C.; Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete, A;Reference number: A71250; MUD:98332770; PMID:9665876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 GYDPKSALVEGKLELDETGYIPTDDNWKTNVEGVFAAGDIRVKSLRQVVTATADGALAAV 303
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                                                                                                                                                                                                                                                                                                                                                                                                                         66 TKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable thioredoxin reductase (trxB) - syphilis spirochete
C.Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C.bate: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                    7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPG-FEMITGPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 LQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDG-----SEETHEADGVFIYI
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                 Length 315;
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                                                                                                                                                                                                                                                                              98; Indels
                                                                                                                                                                                                                           ; DB 1;
1.5e-45;
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46.1%; Pred. No. 6.2e-45;
live 55; Mismatches 108;
                                                                                                                                                                                                                                                                         53; Mismatches
                                                                                                                                                                                                        42.5%; Score 706;
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Matches 142; Conservative
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                                                                                                                                                                                                                                           Similarity
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Matches 150;
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A; Residues: 1-307
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Lincoloxine reductase [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C; Accession: B97007 C; Accession: B97007 Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, F, Molling, J.; Breton, G; Omelchenko, M.V.; Smith, D.R. Gacteriol. 183, 4823-4838, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MUID:21359325; PMID:21359325 A; Accession: B97007 A; Ascession: B97007 A; Ascession: DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeque DNA A; Analeq
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C; Complex: homodimer; each chain has a tightly associated but noncovalently bound C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S29117
R;Mathieu, I.; Mayer, J.; Moulis, J.M.
Biochem. J. 285, 255-262, 1992
A;Title: Cloning, sequencing and expression in Escherichia coli of the rubredoxin sa;Afelerence number: S29117; MUID:92344580; PMID:1637309
A;Accession: S29117
A;Accession: S29117
A;Accession: S29117
A;Residues: I-308 MMATP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE001437; PIDN:AAK78845.1; PID:g15023764; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
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C;Species: Clostridium pasteurianum
C;Date: 06-Nov_1998 #sequence_revision 06-Nov-1998 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.4%; Score 671;
ilarity 42.2%; Pred. No. 6:
Conservative 74; Mismatch
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A,Gene: CAC0869
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A;Molecule type: DNA
A;Residues: 1-317 <ARN>
A;Cross-references: GB:AE001753; GB:AE000512; NID:g4981397; PIDN:AAD35951.1; PID:g498146
A;Experimental source: strain MSB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hit
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
F;14-316/Domain: thioredoxin reductase homology <TRXB>
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Pred. No. 3.9e-44;
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Best Local Similarity 44.8%;
Matches 134; Conservative 6
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F;136-139/Disulfide\ bonds: redox-active #status predicted
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Query Match Best Local Similarity 43.8%; Score 668; DB 1; Length 308; Matches 134; Conservative 64; Mismatches 106; Indels 2; Gaps	1 MGTEIDFDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMIT 60	61 GPDLSTKMFEHAKKFGA-VYQYGDIKSVEDKGEVKVINFGNKELTAKAVIIATGAEVKKI 119 	120 GVPGEQELGGRGVSYCAVCDGAFFRNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDE 179	180 LRAQRILQDRAFKNDKIDFIWSHTIKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIXI 239	240 GMKPLTAPFKDLGITUDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ 299 .	300 SAAEYI 305 : 300 MAEKYI 305	
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Search completed: September 15, 2004, 12:21:32 Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 15, 2004, 12:05:08 , Search time 23 Seconds (without alignments) 724.454 Million cell updates/sec Run on:

US-09-825-212-1

1662 1 MGTEIDFDIAIIGAGPAGMT......AAEYIEHLNDQARSHHHHHH 320 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	099v12 stanhvlococ	8cnv8 s	P80880 bacillus su	928b5 listeria	listeria	50971 eubacteri	52213	83790			092102 ricketters			DESCRIPTION DESCRIPTION	09zd97 ricketteia					O928m4 Chlamidia n		arabidons.			mycoplasma		O9kss4 vihrio obol		highness	00110	47249 miggalage	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	UMPI/1 ureaplasma	1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
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                                           R PIR, E89649; E89849.

R HSSP, Q39243; 1VDC.

R HSSP, Q39243; 1VDC.

R SWISS-2DPAGE; Q99VL2; STAAN.

R INTEFPO; IPRO000759; Adradx reductase.

R INTEFPO; IPRO01327; FAD_DY_redox.

R INTEFPO; IPRO01031; Pyridine_redox_2.

R INTEFPO; IPRO0103; Pyridine_redox_2.

R INTEFPO; IPRO0103; Pyr redox_2 AS.

R INTEFPO; IPRO0109; Pyr redox_1.

R PRINTS; PRO0419; ADKNDTASE.

R PRINTS; PRO0469; PUNBUTASE.

R PRINTS; PRO0469; PUNBUTASEII.

R PRINTS; PRO0469; PUNBUTASEII.

R PRINTS; PRO0459; PUNBUTASEII.

R PRINTS; PRO0573; PYREDINB. REDOX_2; 1.

R PROSTITE; PRO0573; PYREDINB. REDOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
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FAD (FLAVIN PART) (BY SIMILARITY)
1A337DE3736C9265 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  FAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.2%; Score 1582; DB 1; Length 311; 99.4%; Pred. No. 3.1e-107; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (B STAEP TAKE)
TRKE STAEP STAUL.
(G8CPW STAEP 61 43, Created)
F 15-MAR-2004 (Rel. 43, Last sequence update)
T 15-MAR-2004 (Rel. 43, Last sequence update)
JT 15-MAR-2004 (Rel. 43, Last annotation update)
T 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                33616 MW;
              EMBL; AP003131; BAB41952.1; -. EMBL; AP004824; BAB94591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 99.4
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYIEHLNDQA 312
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137
286
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STRAIN=ATCC 12228;
PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                  311 AA;
                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
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TRXB STAEP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 DLSTKWFEHAKKFGAEYQYGDIKSVEDKGDYKVINLGNKEITAHAVIISTGAEYKKIGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEQELGGRGYSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGOMANTEEVENFPGFEMITGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                            pond.
                                                          -1. COFACTOR: Binds 1 FAD per subunit (By similarity).
-1. SUBUNIT: Homodimer (By similarity).
-1. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1. MISCELLANBOUS: The active site is a redox-active disulfide bor -1. SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AE016745; AA004144.1; -.

R InterPro; IPR0010759; Adrndx_reductase.

R InterPro; IPR00103; Pyrir tedox.

R InterPro; IPR00103; Pyridine_redox_2.

R InterPro; IPR008255; Pyr redox_1.

R PRINTS; PR000419; ADXPUTASE.

R PRINTS; PR00461; ADXPUTASE.

R PRINTS; PR00469; PADPNR.

R PRINTS; PR00469; PNDROTASE.

R PRINTS; PR00469; PNDROTASE.

R PRINTS; PR00469; PNDROTASEI.

R TIGRRAMS; TIGR01292; TRX reduct; 1.

R PROSITE; PS00573; PYRIDINE_REDOX_2; 1.

R REdox_active_center; Oxidoreductase; NADP; Flavoprotein; FAD;
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REDOX.ACTIVE (BY SIMILARITY).
PAD (FLAVIN PART) (BY SIMILARITY)
DSD6653667137D8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.5%; Score 1455; DB 1; Length 310; 90.3%; Pred. No. 4.6e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
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Last sequence update)
Last annotation update)
                + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315
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Mol. Microbiol. 49:1577-1593(2003).
-:- CATALYTIC ACTIVITY: Thioredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 AA; 33544 MW;
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RA Kunst F., Ogasawara N. Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.
RA Deceded V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D. Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Göffeau A., Galistin R., Henaut A.,
RA Ghim S.Y., Glaser P., Göffeau A., Galightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Mones L.,
RA Koris B., Karamara D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nuback M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Purnelle B., Ropport G., Rey M., Reynolds S.,
RA Scholin A., Taconi E., Roche E., Rapoport G., Rey M., Reynolds S.,
RA Schoul J., Sekowska A., Seror S.J., Serror P., Schleich S., Schroeter R., Scoffone F.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Tosmoni A.,
RA Tosato V., Wanderbol M., Vannier F., Tosmoni A.,
Winters P., Winter S., Wedler H., Weitzeneger T., Rak Tosato V., Wanderbol M., Vandenbol M., Vannier R., Vasarotti A.,
RA Tosato V., Wandenbol M., Vandenbol M., Vannier R., Vasarotti A.,
RA Tosato V., Wandenbol M., Vannier R., Vashida K., Yoshikawa H., Danchin A.,
Ra Kalitis R., Wander S., Wandenbol M., Vannier R., Vashikawa H., Danchin A.,
Ra Kalitis R., Wander S., Wandenbol M., Vannier R., Vashikawa H., Danchin A.,
Rati R., Wandel P., Vashikawa H., Danchin A.,
Rati R., Wandel P., Wandel P., Vashikawa H., Danchin A.,
Rati R., Wandel P., Wandel P., Wandel P., Wandel P., Wandel P., Wandel P., Wandel P., Wa
      (EC 1.8.1.9) (TRXR) (General stress protein 35)
                                                                                                                                                                                                   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                      Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390:249-256(1997).
      Thioredoxin reductase
                                                                                 Bacteria; Firmicutes;
NCBI_TaxID=1423;
                                                            Bacillus subtilis.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                              OR BSU34790
                                                                                                                                                               STRAIN=168;
                                                                                                                                                                                                                                                                      STRAIN=168;
                                                                                                                                                                                      Denizot F.
                                              TRXB
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"First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtills.";
Electrophoresis 18:1451-1463(1997)
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                       STRAIN=168 / ISS8,
MEDLINE=97443988; PubMed=9298659;
Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
SEQUENCE OF 1-23
                                                                                                                                Hecker M.;
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-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-:- INDUCTION: By heat shock, salt stress, oxidative stress, glucose
limitation and oxygen limitation
-:- MISCELLANEOUS: The active site is a redox-active disulfide bond (By similarity). -!- COFACTOR: Binds 1 FAD per subunit (By similarity). oxidoreductase family.

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                                                                                                                                                                                                                                                                                                     134 137 REDOX-ACTIVE (BY SIMILARITY).
277 286 FAD (FLAVIN PART) (BY SIMILARITY).
1 5 - A (IN REF. 3).
5 6 7 -> E (IN REF. 3).
315 AA; 34388 MW; 1BED957C979AE2AC CRC64;
                                                                                                                                                                                  PRINTS; PRO0368; FADDR.
PRINTS; PRO041; PNDRDTASEI.
PRINTS; PRO0461; PNDRDTASEI.
TIGREAMS; TIGR01222; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                           FAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                     Length 315;
                                                                                                                                                                                                                                                                                                                                                                              69.4%; Score 1154; DB 1; Length 3 71.4%; Pred. No. 2.5e-76; live 33; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCEL TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update
Thioredoxin reductase (EC 1.8.1.9) (TRXR)
                                            PIR; A69727; A69727.
HSSP, Q39243; IVDC.
Subtilist, BG12399; trxB.
InterPro; IPR000759; Adrndx reductase.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR00100; Pyr_redox.
InterPro; IPR008255; Pyr_redox.
InterPro; IPR008255; Pyr_redox.2.
InterPro; IPR008292; Thioredox_reduct.
Pfam; PF00070; pyr_redox; 1.
PRINTS; PR00419; ADXRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319
  email to license@isb-sib.ch)
                      EMBL; Z94043; CAB08055.1; -. EMBL; Z99121; CAB15484.1; -.
                                                                                                                                                                                                                                                                                                                                                                          Query Match 69.4%
Best Local Similarity 71.4%
Matches 220; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 ELQETLKT 313
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DISULFID
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CONFLICT
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HSSP; 039243;
Listilist; LM002478; -...ndx_reductase.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
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                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                             HLND 310
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STRAIN=CLIP 11262 / Serovar 6a;

MEDLINE=21537279; PubMed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

A Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Cherbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Brian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

A Gutier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

A Jones L.-M., Kaerset U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsieß G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Nazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
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                                                                                                                                                                                                                                                                                                               Science 294:849-852(2001).
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                        -:- COFACTOR: Binds 1 FAD per subunit (By similarity).
-:- SUBLUIT: Homodimer (By similarity).
-:- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-:- MISCELLANBOUS: The active site is a redax-active disulfide bond.
-:- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
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PROSITE; PS00573; PYRIDINE REDOX 2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAD (ADP PART) (BY SIMILARITY). REDOX-ACTIVE (BY SIMILARITY). PAD (FLAVIN PART) (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.6%; Score 1057; DB 1; Length 319; 65.8%; Pred. No. 2.6e-69;
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LinterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001103; Pyridine_redox_A:
InterPro; IPR005982; Thioredox_reduct.
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PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
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PRINTS; PR00469; PNDRDTASEII
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(X) STAINEGOLE / Serovar 1/2a;

(X) GIASEL P. Frangeul L., Buchrieser C., Rusniok C., Amend A.,

(A) Claser P., Frangeul L., Buchrieser C., Randt P., Chakraborty T.,

(X) Bardhe P., Bloecker H., Brandt P., Chakraborty T.,

(X) Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

(X) Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

(X) Domann E., Cominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

(X) Bartier L., Goobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

(X) Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

(X) Andueno E., Maitournam A., Mara Vicente J., Ng E., Nedjari H.,

(X) Nordsiek G., Novella S., de Pablos B., Perez-Dlaz J.-C., Purcell R.,

(X) Remmel B., Rose M., Schlueter T., Simose N., Tierrez A.,

(X) Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

(X) Comparative genomics of Listeria species.";
188 QDRAFKDEKVDFIWNNTVEEIIGDGKKVTSVKLVSTVDGSESIMPVDGVFIYVGLVPLTK 247
                                                                                                                                             248 AFLSLGITDEEGYIVTDEEMRTNLPGIFAAGDVRAKSLRQIVTATGDGGLAGONAQXYVE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-EGD / Serovar 1/2a;
Borovok I., Mislovati M., Cohen G., Aharonowitz Y.;
"Isolation, cloning and characterization of the Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294:849-852(2001).
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                 247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAABYIE
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
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SAAEYIE 306
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                    SEQUENCE OF 1-54.
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                                                                                                                                                                                                                                                                                                                 QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSBETHEADGVFIYIGMKPLTA 246
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                                                                                                                                                                                                                                                                                                                                                                                                248 AFLNLGITDDEGYIVTDEEMRINLPGIFAAGDVRAKSLRQIVIATGDGGLAGQNAQKYVE 307
                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                         7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
                                                                                                                                                                                                                                     Luebbers M., Andreesen J.R., "Components of glycine reductase from Eubacterium acidaminophilum. Cloning, sequencing and identification of the genes for thioredoxin reductase, thioredoxin and selenoprotein PA."; Elochem. 217:791-798(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eubacterium acidaminophilum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
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                                                                                                                                  FAD (ADP PART) (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY); 8D42F36970611979 CRC64;
                                                                                         TIGRFAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRLDINE REDOX 2; 1.
Redox-active center; Oxidoreductāse; NADP; Flavoprotein; FAD;
Complete proteome
                                                                                                                                                                                   Query Match
63.4%; Score 1054; DB 1; Length 319;
Best Local Similarity 65.5%; Pred. No. 4.3e-69;
Matches 199; Conservative 43; Mismatches 62: Indele
                                                                                                                                                                                                          62; Indels
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Andreesen J.R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                              ; Pred. No. 4.3e-69; 43; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 AA
InterPro; IPR000103; Pyridine_redox_2.
InterPro; IPR003042; Rng_mnoxygenase.
InterPro; IPR005982; Phioredox_reduct.
Pfam; PF00070; pyr_redox; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00419; PADPR.
PRINTS; PR00461; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEI.
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MEDLINE=94039119; PubMed=8223622;
                                                                                                                                  44 FAJ
139 REJ
288 FAJ
7 34173 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eubacterium.
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P50971;
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                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                                    89
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                              187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 ELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 LQDRAFKNDKIDFIWSHTTKSINEKDGKVGS-----VTLTSTKDGSEETHEADGVFIYI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
MEDITALE 89155433; PubMed=2537814; MEDertz H., Andreesen J.R.; Freundenberg W., Dietrichs D., Lebertz H., Andreesen J.R.; Freundenberg W. an atypically small lipoamide dehydrogenase involved in the glycine decarboxylase complex from Eubacterium acidaminophilum."; J. Bacteriol. 171:1346-1354(1989).
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                                                                                                                                                                                                                                                                  -:- SUBUNIT: Homodimer (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- MISCELLANBOUS: The active site is a redox-active disulfide bond.
-:- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RINGEPTO: IPRO00759; Adrindx reductase.

RINGEPTO: IPR000759; Adrindx reductase.

RINGEPTO: IPR0001327; FAD_DYT_redox.

RINGEPTO: IPR0001100; PYT_redox.

RINGEPTO: IPR0008255; PYT_redox2_AS.

RINGEPTO: IPR000825; PYT_redox2_AS.

RINGEPTO: IPR005982; Thioredox_reduct.

RINTES: PR00070; PYT_redox_reduct.

RRINTS: RR00419; ADXENTASE.

RRINTS: PR001919; ADXENTASE.

RRINTS: PR001919; ADXENTASE.

RRINTS: PR001919; ADXENTASE.

RRINTS: PR001919; ADXENTASE.

RRINTS: RR00469; PRNDFASEI.

RRINTS: RR00469; PRNDFASEI.

RRINTS: RR00469; PRNDFASEI.

RRINTS: RR00469; PRNDFASEI.

RRINTS: RR00469; PRNDFASEI.

RROSTIE; PR006073; PYRIDINE REDOX 2; 1.

RR00774; RR00775; RR0076477; RR PR0 (ADP PART) (BY SIMILARITY).

TO ISULED 134 137 REDOX-ACTIVE (BY SIMILARITY).

TO PRIND 2282 291 REDOX-ACTIVE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.7%; Score 726; DB 1; Length 31
49.8%; Pred. No. 2e-45;
iive 50; Mismatches 96; Indels
                                                                                                                                                                                                                                      -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145B0EABB2B8A7FA CRC64;
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315 AA; 34033 MW;
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HSSP; P09625; 1TDE.
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TRXB OR TP0814
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                                                                                                                                                                                                                                                                                                                                         Kreimer S., Andreesen J.R.;
"Glycine reductase of Clostridium litorale. Cloning, sequencing, and
"Glycine reductase of Clostridium litorale. Cloning, sequencing, and
molecular analysis of the grdAB operon that contains two in-frame TGA
codons for selenium incorporation.";
Bur. J. Biochem. 234:192-199(1995).
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- COFACTOR: Binds 1 FAD per subunit (By similarity).
-:- SUBUNIT: Homodimer (By similarity).
-:- SUBCELIALIZE LOCATION: Cytoplasmic (By similarity).
-:- SUBCELIANEOUS: The active site is a redox-active disulfide bond.
-:- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HISSP, 039249; 1VDC.

R InterPro; IPR001327; FAD pyr redox.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR001100; Pyr_redox.

R InterPro; IPR001010; Pyr_redox.

R InterPro; IPR001013; Pyr_redox.

R InterPro; IPR001019; Pyr_redox.

R InterPro; IPR001019; Pyr_redox.

R InterPro; IPR001019; Pyr_redox.

R PRINTS; PR00419; ADXRDTASE.

R PRINTS; PR00419; ADXRDTASE.

R PRINTS; PR00419; PNDRDTASEI.

R PRINTS; PR00419; PNDRDTASEI.

R PRINTS; PR00419; PNDRDTASEI.

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R PRINTS; PNDRDTASEI.

R PRINTSE
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8
                                                                                                                                                                                                  Clostridium litorale (Bacterium W6).
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.5%; Score 706; DB 1; 48.5%; Pred. No. 5.6e-44;
                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Mismatches
                                                                  315 AA
                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MCT-2004 (Rel. 43, Last amnotation update
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=96096738; PubMed=8529640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U24268; AAC43575.1; -.
PIR; S63990; S63990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 150; Conservative
                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                     NCBI_TaxID=1557;
                                                                                                                                                                                                                                                      Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         + NADPH
                                                                      CLOLI
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                                                                                                                                                                                 240 GMKPLTAPPKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ 299
                                                                                                                                                                                                                                                                                                                              244 GYDPKSALVEGKLELDETGYIPTDDNMKTNVEGVFAAGDIRVKSIRQVYTATADGAIAAV 303
                                                MEDLINE=98332770; PubMed=9665876, Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., Hach B., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Artiach P., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
ELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEBGTFTTKFADKVTIVHRKDELRAQRI
                                                                                                                                         LODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDG-----SEETHEADGVFIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBL_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBGUNIT: Homodimer (By similarity)
-i- SUBGLIULAR LOCATION: (Sypolasmic (By similarity)
-i- SUBCELLANEOUS: The active site is a redox-active disulfide bot
-i- MINCELLANEOUS: The active site is a redox-active disulfide
-i- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR00103; Pyr_redox2.
InterPro; IPR00103; Pyridine_redox2.
InterPro; IPR005982; Thioredox_reduct.
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PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             300 SAREYIEHL 308
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HSSP, Q39243, 1VDC.
TIGR, TP0814; -
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us-09-825-212-1.rsp

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RESULT 10
TRXB STRCL
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                                                                                                                                                                                                                                            63 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP 122
                                                                                                                                                                                                                                                                                               GEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRA 182
                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                QRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSETHEADGVFIYIGMK 242
                                                                                                                                                                                                                                                                                                                                                                                                   PLTAPFKDLGIINDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                    241 PITGLLPD-AEKDSTGYIVTDDEMRTSVEGIFAAGDVRAKSFRQVITATSDGALAAHAAA 299
                                                                                                                                                                                          4 EIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEM-ITGP 62
                                                                                                                                                                                                                  ETDYDVIIVGAGAAGLSAAQYACRANLRTLVIESKAHGGQALLIDSLENYPGYATPISGF 61
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rubredoxin gene from Clostridium pasteurianum.";
Biochem. J. 285.255-262(1992)
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                          3,
    PRINTS; PRO0469; PNDEDTAGEI.

TIGREAMS; TIGR01292; TRX_reduct; 1.

PROSITE; PS00573; PYRIDINE_REDOX 2; 1.

Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD; NADP PROTECTION PROPERTY.
                                                                                FAD (ADP PART) (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
2519A5BA3BB4E012 CRC64;
                                                                                                                                           42.0%; Score 697.5; DB 1; Length 307; 46.1%; Pred. No. 2.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92344580; PubMed-1637309;
Mathieu I., Meyer J., Moulis J.M.;
"Cloning, sequencing and expression in Escherichia coli of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.2 kDa protein in rubredoxin operon (EC 1.6.4.-) (ORF A) Clostridium pasteurianum.
                                                                                                                                                     Best Local Similarity 46.1%; Pred. No. 2.2e-43;
Matches 142; Conservative 55; Mismatches 108; Indels
                                                                             FAD (ADP PART) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                   32868 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
 PR00411; PNDRDTASEI. PR00469; PNDRDTASEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M60116; AAA23276.1; -. PIR; S29117; S29117.
HSSP; Q39243; 1VDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                             41
137
284
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                                                                                                               307 AA;
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SEQUENCE FROM N.A.
                                                                             34
134
275
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NCBI_TaxID=1501;
                                                                                       DISULFID
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLOPA
                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                123
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                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                183
                                                                             BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R34K_CLOPA
ID R34K_CLO
AC P23160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GADLADKWEBHAASIGVNIDQFSNIEKIKLSDDEKIIETEDVIYKVKALIIATGAKSRRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GVPGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSBETHEADGVFIYI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 GMKPLTAPFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                 09
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InterPro; IPR000759; Adrndx reductase.

R InterPro; IPR001327; FAD_pyr_redox.

R InterPro; IPR001327; FAD_pyr_redox.

R InterPro; IPR00103; Pyr_redox.

R InterPro; IPR008055; Pyr_redox.

R Ffam; PR000103; Pyridine_redox.

R Pfam; PR00010; pyr_redox.

R PRINTS; PR00411; PNDRDTASE.

R PRINTS; PR00469; PNDRDTASEI.

R PRINTS; PR00469; PNDRDTASEII.

R PRINTS; PR00469; PNDRDTASEII.

R PROSTIE; PS00573; PYRIDINE_REDOX 2; 1.

R PROX-active center; Oxido_eductase; NADP; NAD; Flavoprotein; FAD.

T DISULID 136 139

T NP FIND.
                                                                                                                                                                                                                                                                                                                                                                                                   1 MGTEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMIT
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Thioredoxin-thioredoxin reductase system of Streptomyces clavuligerus: sequences, expression, and organization of the J. Bacteriol. 175:5159-5167(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aharonowitz Y., Av-Gay Y., Schreiber R., Cohen G.;
"Characterization of a broad-range disulfide reductase from
                                                                                                                                                                                                                                                                                                                  Query Match
40.2%; Score 668; DB 1; Length 30
Best Local Similarity 43.8%; Pred. No. 3e-41;
Matches 134; Conservative 64; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 1-32.
STRAIN=ATCC 27064 / DSM 738 / NRRL 3585,
MEDLINE=93352422; PubMed=8349555;
Cohen G., Yanko M., Mislovati M., Argaman A., Schreiber
Av-Gay Y., Aharonowitz Y.;
                                                                                                                                                                                                                                                                              308 AA; 34215 MW; 52D9CF51208EFC37 CRC64;
                                                                                                                                                                                                                                                                  FAD (FLAVIN PART)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-07N-1994 (Rel. 29, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE=93139027; Pubmed=8423136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 SAAEYI 305
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NP BIND
SEQUENCE
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+ NADPH
                                               RICCN
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                                                          092102;
                        RESULT 11
TRXB_RICCN
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 TKMPEHAKKFGAVYQYGDIKSVEDKGEYK-VINFGNKELTAKAVIIATGAEYKKIGVPGE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 QELGGRGVSYCAVCDGAFFKNKRLFVIGGDSAVEEGTFTTKFADKVTIVHRRDELRAQR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAPFKDLGITNDVGYI-VTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 TELFKGQLDLDDEGYLKVASPSTRTNLTGVFAAGDVVDHTYRQALTAAGTGCSAALDAER 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 DIAIIGAGPAGMTAAVYASRANLKTVMIERGI-PGGQMANTEEVENFPGF-EMITGPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                               disulfide redox balance.
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                              -:- SUBUNIT: Homodimer.
-:- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-:- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                         J. Bacteriol. 175:623-629(1993).
-1- FUNCTION: Component of the thioredoxin-thioredoxin reductase system which may be involved in biosynthesis of penicillins at cephalosporins and may be important in determining the thiol-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REDOX-ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY)
4C2B01AADC5A0FDF CRC64;
Streptomyces clavuligerus and its possible role in beta-lactam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.8%; Score 644.5; DB 1; Length 321; 45.6%; Pred. No. 1.6e-39; tive 53; Mismatches 109; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIGRFAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAD (ADP PART) (BY SIMILARITY).
                                                                                                               -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001327; PAD_pyr_redox.
InterPro; IPR001805; Pyr_redox.
InterPro; IPR008255; Pyr_redox2.
InterPro; IPR000139; PyrIdine_redox2.
InterPro; IPR005982; Thioredox_reduct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 AA; 34015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII
                                                                                                                                                                                                                                                                                       EMBL; Z21946; CAA79940.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00070; pyr redox; 1 PRINTS; PR00419; ADXRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 140; Conservative
                antibiotic biosynthesis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 YLAALAD 310
                                                                                                                                                                                                                                                                                                    PIR; A53307; A53307.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                HSSP; P09625; 1CLO.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
-:- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: Homodimer (By similarity).
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- MISCELLEANEOUS: The active site is a redox-active disulfide bond.
-i- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Ogata H., Audic V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 41 FAD (ADP PART) (BY SIMILARITY).
135 138 REDOX-ACTIVE (BY SIMILARITY).
281 290 FAD (FLAVIN PART) (BY SIMILARITY)
310 AA; 33469 MW; 0F1E04D6BC7E111B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 310;
                                                                                                                                                                                                             Rickettsia conorii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAM; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE REDOX 2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: Binds 1 FAD per subunit (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.6%; Score 641.5; DB 1;
46.0%; Pred. No. 2.5e-39;
tive 45; Mismatches 107;
                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
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310 AA
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InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001355; Pyr_redox.2.
InterPro; IPR001359; Pyr_redox.2.
InterPro; IPR005981; Thioredox_reduct.
Pfam; PF00070; pyr_redox; I.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00461; PADRUTASEI.
PRINTS; PR00461; PNDRUTASEI.
                                                                                                                                                                                                                                                                     Rickettsiaceae; Rickettsieae; Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE008622; AAL03156.1; -. PIR; B97777; B97777.
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Matches 144; Conservative
   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAD (ADP PART) (BY SIMILARITY)
REDOX-ACTIVE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGREAMS; TIGRO1222; TEX reduct; 1.
PROSITE; PSO0573; PYRIDINE_REDOX_2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Mismatches 104; Indels
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V -> C (IN REF. 1)
V -> Y (IN REF. 1).
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46.4%; Pred. No. 3.9e-39;
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                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist, Rv3913;
InterPro, IPR000759; Adrndx reductase.
InterPro, IPR001327; FAD_Dyr_redox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR01100; Pyr_redox.
InterPro; IPR001100; Pyr_redox2 As.
InterPro; IPR000103; PyrIndox2 As.
InterPro; IPR000103; PyrIdine_redox 2.
InterPro; IPR005982; Thioredox_reduct.
PFam; PR00070; pyr_redox; 1.
PRINTS; PR00419; ADXRDTASE.
                                                                                                                                                                                                                                                                           EMBL, AL021426; CAA16226.1; -.
EMBL, AAE007194; AAK48397.1; -.
PIR; A70851; A70851
HSSP, Q39243; 1VDC.
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PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
                     oxidoreductase family.
                                                                                                                                                                                                                                                   EMBL; X95798; CAA65070.1;
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335 AA;
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                                             122 PGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELR 181
                                                                                                                                                                               AEKILODRIFKNSKISVIMDHVVDEI-----VGSNKPKSVTGVKIQNVHTKEISLINCS 235
                                                                                                                                                                                                                             GVFIYIGMKPLTAPFKDLGITNDVGYIVTKDDMT-ŢSVPGIFAAGDVRDKGLRQIVTATG 292
                                                                                                                                                                                                                                                            62 WLMEQMYMQAKNVGTEIVSDYVEKVDLSKRPFKVFTGAGNEYDAESIIICTGAEAKWLGI 121
                                                                     182 AQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGS---VTLTSTKDGSEETHE----AD
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-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis and funtional characterization of thioredoxin and thioredoxin reductase of Mycobacterium tuberculosis.", Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=H3RV;
MEDLINE=98295987; PubMed=9634230;
COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd E., Hernsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Hornsby T., Cohorn J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wieles B., Phillip W., Drijfhout J.W., Offringa R., Ottenhoff T.H.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRXB MYCTU STANDARD, PRT; 335 AA. P5214; 053592; 01-0CT-1996 (Rel. 34, Created) 15-JUL1999 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Thioredoxin reductase (EC 1.8.1.9) (TRXR) (TRX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                           DGSIAAQSAAEYI 305
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SEQUENCE FROM N.A.
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InterPro; IPR005746; Thioredoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Bifunctional thioredoxin reductase/thioredoxin [Includes: Thioredoxin reductase (EC 1.8.1.9) (TRXR); Thioredoxin].
TRXB/A OR TRX OR ML2703.
                                                                                                                                                                                    MEDILINE=97124199; PubMed=8968512; Reihi H., de Rossi E., Salazar L., Cantoni R., Labo M., Riccardi G., Takiff H.B., Eiglmeier K., Bergh S., Cole S.T.; Gles Trangement and organization in an approximately 76 kb fragment encompagning the oriC region of the chromosome of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                   "Unique gene organization of thioredoxin and thioredoxin reductase in Mycobacterium leprae.";
Mol. Microbiol. 16:921-929(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: The active site is a redox-active disulfide bon
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                                                                          Wieles B., van Soolingen D., Holmgren A., Offringa R., Ottenhoff
                                                                                                              Bācteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxidoreductase family. SIMILARITY: Belongs to the thioredoxin family.
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InterPro; IPR001327; FAD pyr redox.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001035; Pyr redox2 AS.
InterPro; IPR00103; PyrIdine_redox_2.
InterPro; IPR06663; Thiored.
InterPro; IPR06663; Thioredox dom2.
InterPro; IPR006693; Thioredox_reduct.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=96059638; PubMed=7476189;
                                                                                                                                                                                                                                                                                  Microbiology 142:3147-3161(1996)
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EMBL; X87899; CAA61150.1; -.
                                                                                                      Mycobacterium leprae.
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                                                                                                                                                                                SEQUENCE FROM N.A.
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67 KMFEHAKKEGAVYQYGDIKSVEDKGEYK-VINFGNKELTAKAVIIATGAEYKKIGVPGEQ 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLVSDVVDIDPDGYVLVKGRTTSTSMDGVFAAGDLVDRTYROAITAAGSGCAAAIDAERW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 DIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEM-ITGPDLST 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 APFKDLGITNDVGYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 LQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLT
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MEDLINE=99014240; PubMed=9795152;

Gal-Mor O., Borovok I., Av-Gay Y., Cohen G., Aharonowitz Y.;

Gene organization in the trxA/B-oriC region of the Streptomyces

coelicolor chromosome and comparison with other eubacteria.";

Gene 217:83-90(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                          458 THIOREDOXIN.
48 FAD (ADP PART) (BY SIMILARITY).
145 REDOX-ACTIVE (BY SIMILARITY).
294 FAD (FLAVIN PART) (BY SIMILARITY).
382 REDOX-ACTIVE (BY SIMILARITY).
49046 MW; 84D367AB31899987 CRC64;
                           PRIMTS; PRO0419; ADXEDTASE.
PRINTS; PRO0368; PADNETASE.
PRINTS; PRO0411; PNDRDTASEI.
PRINTS; PRO04211; PHORDTASEI.
PRINTS; PRO0421; THOREDOXIN.
TIGREAMS; TIGRO1068; thioredoxin; 1.
TIGREAMS; TIGRO1292; TRX reduct; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PSO0194; THOREDOXIN; 1.
PROSITE; PROME THOREDOXIN; 1.
PROSITE; PROME THOREDOXIN; 1.
PROSITE; PROME THOREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.1%; Score 632.5; DB 1; Length 458; 45.3%; Pred. No. 1.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                            Complete proteome.
321 THIOREDOXIN REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
                                                                                                                                                                                                                                                                                                                                                               LINKER
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Pfam; PF00070; pyr_redox; 1.
Pfam; PF00085; thiored; 1.
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142
285
379
458 AA;
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Matches 140; Conserv
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DISULFID
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DISULFID
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Similarity
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                Query Match
Best Local S
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TRXB_RICPR
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FAD (ADP PART) (BY SIMILARITY).

FREDOX-ACTIVE (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

A -> R (IN REF. 1; CAA63075/CAA07451).

ER -> DG (IN REF. 1; CAA63075/CAA07451).

MISSING (IN REF. 1; CAA63075).

G -> A (IN REF. 1; CAA63075).

MISSING (IN REF. 1; CAA63075).

V -> L (IN REF. 3).

P -> R (IN REF. 3).
                                                                                                        STRAIN=A3(2) / M145;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed K.D. Touring G.L., Reser H. Harris D.E., Quail M.A., Kieser H., Goble A., Hidalgo J., Hornsby T., Howarth S., Rubbinowitsch E., Rajandream M.A., Rutherford K., O'Neil S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                             xr = 41/:141-14/(2002).
CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Homodimer (By similarity)
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-!- MISCELLANEOUS: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).", Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PVRIDINE REDOX 2; 1.
Redox-active center; Oxidoreductase; NADP; Flavoprotein; FAD;
                                                   Aharonowitz Y.,
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3A829A566A8345AE CRC64;
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EWBL; X92104; CAA63076.1;

EWBL; AJ007313; CAA63075.1;

EWBL; AL939118; CAA67451.1;

EWBL; AL939118; CAA67451.1;

EWBL; AL939118; CAA642713.1;

PIR; T42062; T42062.

HSSP; Q39243; 1VDC.

INCEPPO; IPR001759; Adrndx reductase.

INCEPPO; IPR001307; PAD Pyr redox.

INCEPPO; IPR001300; Pyr redox.

INCEPPO; IPR00100; Pyr redox.

INCEPPO; IPR00100; Pyr redox.

INCEPPO; IPR00100; Pyr redox.

INCEPPO; IPR00100; Pyr redox.

INCEPPO; IPR00100; Pyr redox.

INCEPPO; IPR00100; Pyr redox.

INCEPPO; IPR00100; Pyr redox.

INCEPPO; IPR00100; Pyr redox.

PR NATS.
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34024 MW;
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PRINTS; PRO0411; PNDRDTASEI.
PRINTS; PRO0469; PNDRDTASEII
TIGRFAMS; TIGR01292; TRX redi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0419; ADXRDTASE.
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138
287
25
73
154
                                  STRAIN=A3(2) / M145;
                                                                                               SEQUENCE FROM N.A
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INIT MET 0
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135
278
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72
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303
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REVISIONS.
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NP_BIND
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                                                                                                                                                                                                                                                                                                  185 ILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEFTHEADGVFIYIGMKPL 244
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                                                                                                                                                                                                                                               TAPFKDLGITNDVGYI-VTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAE 303
                                                                                                                                                                                                                                                                                                                                                                                                      244 TELFKGQLDLDPBGYLKVDAPSTRINLTGVFGAGDVVDHTYRQAITAAGTGCSAAVDAEP 303
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                                                                                                                       64
                                                                      8 DIAIIGAGPAGMTAAVYASRANLKTVMIERGI-PGGQMANTEEVENFPGF-EMITGPDLS
                                                                                                         5 NVIIIGSGPAGYTAALYTARASLKPLVFEGAVTAGGALMNTTEVENFPGFQDGIMGPELM
                                                                                                                                                                      mitochondria.";
Nature 396:133-140(1998).
-!- CATALYTIC ACTIVITY: Thioredoxin + NADP(+) = thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
-!- SUBGNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- MISCELLANEOUS: The active site is a redox-active disulfide bon
-!- SIMILARITY: Belongs to class-II pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K. Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                               5
         Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria, Rickettsiales;
37.6%; Score 625.5; DB 1;
43.7%; Pred. No. 3.8e-38;
live 56; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Thioredoxin reductase (EC 1.8.1.9) (TRXR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
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Q9ZD97,
30-MAY-2000 (Rel. 39, Created)
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HSSP; P09625; 1TRB.
                                   Matches 136; Conservative
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us-09-825-212-1.rsp

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237 IYIGMKPLTAPFKDLGITNDVGYIVTKDDMT-TSVPGIFAAGDVRDKGLRQIVTATGDGS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 AORILODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHE-----ADGVF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 PGEQELGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DLSTKMFEHAKKFGAVYQYGDIKSVE-DKGEYKVINFGNKELTAKAVIIATGAEYKKIGV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.3%; Score 619.5; DB 1; Length 310;
45.2%; Pred. No. 9.8e-38;
ative 48; Mismatches 111; Indels 11; Gaps
InterPro; IPR001327; FAD_pyr_redox.

InterPro; IPR001327; FAD_pyr_redox.

InterPro; IPR00100; Pyr_redox.

InterPro; IPR0010103; Pyr_redox.2 AS.

InterPro; IPR00103; Pyr_redox.2.

InterPro; IPR005982; Pyr_redox.2.

InterPro; IPR005982; Pyr_redox.2.

INTERPORT PR00411; PNDRDTASE.

INTERPAMS; PR00411; PNDRDTASEI.

INTERPAMS; TIGR01292; TRX_reduct; 1.

INTERPAMS; TIGR01292; TRX_reduct; 1.

INTERPAMS; TIGR01292; TRX_reduct; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.

INTERPAMS; PR00573; PYRIDINE REDOX.2; 1.
                                                                                                                                                                                                                                                                                   34 41 FAD (ADP PART) (BY SIMILARITY).
135 138 REDOX-ACTIVE (BY SIMILARITY).
281 290 FAD (FLAVIN PART) (BY SIMILARITY)
310 AA, 33582 MW; 573CA975C750957D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.2%
Matches 140; Conservative
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299 MAALEVAKFL 308
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Search completed: September 15, 2004, 12:16:34 Job time : 24 secs

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September 15, 2004, 12:12:53 ; Search time 115 Seconds (without alignments) 877:964 Million cell updates/sec
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1 MGTEIDFDIAIIGAGPAGMT.....AAEYIEHLNDQARSHHHHHH 320
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_barchei:*
sp_hungi:*
sp_hungi:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_phage:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_prodent:*
sp_vortebrate:*
sp_vortebrate:*
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	054079 stanhvlocon	099v12 staphylococ	O9kx07 stanbylogo	Oborge of a business	Gerpye staphy totoc	Corred Dacillus an	Coloji pacilius ce	Vecaya oceanopacil	Q9K/03 bacillus ha	Q88yj/lactobacill	Q835nB enterococcu	Ognzys streptococc	Vakbaz streptococc			Q8e//3 streptococc Q8e1q9 streptococc
SUMMARIES	ID	054079	Q99VL2	Q9KX07	OSCPYS	081X56	0815.11	80X080	O9K703	CO (XC)	00000 00000	OBNOVE	CHREIS	O8DM:7	COLHO	08E773	Q8E1Q9
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	Score	1582	1582	146/	1455	1173	1170	1146	1145.5	943	940	899	897	882	872	852.5	852.5
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Q8DP78 Q97PY2 Q93FC9 Q9EV96	Q8R8V8 Q9RSY7 Q9WZX3	Q97KP8 Q97KP8 Q8G6J1 Q9V0Q8 O50134	Q93AQ4 Q8U108 Q8PU11 Q7TVC8 Q8FSW1	Q9RIS2 Q897A0 Q8NL59 Q8TR16 Q82FE8	Q8EUJ3 29X5F7 026804 Q8XMA7 Q84W20 Q8DHM2
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851 849 815 753 746	741 728.5 687 682.5	671 647.5 645.5 643.5	641.5 639.5 638.5 635.5 634	629.5 626 625.5 613.5	599.5 594.5 594.5 592.5
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ALIGNMENTS

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ORILODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
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I adoct 359:1819-1827(2002).

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I copactor. FAD (BY SIMILARITY).

I copactor. FAD (BY SIMILARITY).

EMBL; AP003306; BAB84591.1;

BMBL; AP004824; BAB94591.1;

BMBL; AP004824; BAB94591.1;

BMSP; Q39243; 1V0C.

G0; G0:005737; C:cytoplasm; IEA.

G0; G0:005737; C:cytoplasm; IEA.

G0; G0:0004791; F:thioredoxin-disulfide reductase activity; IEA.

G0; G0:0004791; F:thioredoxin-disulfide radicals; IEA.

G0; G0:0004791; P:thioredoxin-disulfide radicals; IEA.

InterPro; IPR001327; FAD pyr_redox.

InterPro; IPR001327; FAD pyr_redox.

InterPro; IPR00100; Pyr_redox.

InterPro; IPR00100; Pyr_redox.

InterPro; IPR00100; Pyr_redox.

InterPro; IPR00100; Pyr_redox.

InterPro; IPR00100; Pyr_redox.

InterPro; IPR008255; Pyr_redox.

InterPro; IPR008255; Pyr_redox.

InterPro; IPR008255; Pyr_redox.

InterPro; IPR008255; Pyr_redox.

InterPro; IPR008255; Pyr_redox.

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InterPro; IPR008255; Pyr_redox.

InterPro; IPR008255; Pyr_redox.

InterPro; IPR008255; Pyr_redox.

InterPro; IPR008255; Pyr_redox.
                                                                                                                                                                                       MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.2%; Score 1582; DB 16; Length 311; 99.4%; Pred. No. 2e-104; ive 0; Mismatches 2; Indels 0.
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Pfam; PP00070; pyr redox; 1.
PRINTS; PR00149; ADXRDTASE.
PRINTS; PR00141; PADRDTASEI.
PRINTS; PR00411; PURDTASEII.
PRINTS; PR00469; PNRDTASEII.
TIGRFAMS; TIGR01292; TRX reduct; 1.
TIGRFAMS; TIGR01292; TRX reduct; 1.
FAD; FlavOptocini, Oxidoreductase; Complete proteome.
FAD; FADVOptocini, Oxidoreductase; Complete proteome.
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                                                                                             Lancet 357:1225-1240(2001)
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Best Local Similarity 99.4
Matches 308; Conservative
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                           GO:0015036; F:disulfide oxidoreductase activity; IEA. GO:0004791; F:thioredoxin-disulfide reductase activity; IEA. GO:0006118; F:electron transport; IEA. GO:0019430; P:removal of superoxide radicals; IEA.
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0
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01-OCT-2003 (TYENBLrel. 25, Last annotation update)
Thioredoxine reductase.
Thioredoxine xeductase.
Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain N315).
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NCBI_TaxID=159878, 158879, 196620;
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                                                                                                                           InterPro; IPR000759; Adrada reductase.
InterPro; IPR000759; Adrada reductase.
InterPro; IPR001013; Pyridiane redox_2.
InterPro; IPR001013; Pyridiane redox_2.
InterPro; IPR001010; Pyr redox_2.
InterPro; IPR008255; Pyr_redox_2.
InterPro; IPR008255; Pyr_redox_2.
InterPro; IPR008982; Thioredox_reduct.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00411; PNDRDTASEI.
TIGRFAMS; TIGR01292; TRX_reduct; 1.
PROSITE; PR00573; PYRIDINE_REDOX_2; 1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
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Matches 308; Conserv
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SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
                                                                                                                                                                                 EMBL, AE016745; AA0041441; ..., GO, GO, 10015737; C: Cytoplasm; IEA.
GO, GO: 0015036; F: Gisulfide oxdoreductase activity; IEA.
GO, GO: 0004791; F: Finioredoxin-disulfide reductase activity; IEA.
GO, GO: 0006118; P: electron transport; IEA.
GO; GO: 0019430; P: removal of superoxide radicals; IEA.
                                                                                                                                                                 Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 AA; 33544 MW; D5D6853667137D8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 87.5%; Score 1455; DB 16; Local Similarity 90.3%; Pred. No. 2.1e-95; les 278; Conservative 17; Mismatches 13;
                   Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                            PEAM; PF00070; pyr redox; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00418; PADDRE..
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEI.
TIGRPAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                                                                                                                                                                                                                              InterPro; IPR000759; Adrndx reductase.
InterPro; IPR001327; PAD pyr redox.
InterPro; IPR00103; Pyridine_redox_2.
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001100; Pyr redox.
InterPro; IPR008255; Pyr redox2 AS.
InterPro; IPR005982; Thioredox_reduct.
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DYITELKD 309
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SEQUENCE 310 AA
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01-JUN-2003
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Matches
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Q81X56
1D Q81X
AC Q81X
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                                                                                                                                                                                                                                                                                                                                                       R GO; GO:000573; C:cytoplasm; IEA.

R GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0004731; F:thioredoxin-disulfide reductase activity; IEA.

R GO; GO:0019430; P:electron transport; IEA.

R GO; GO:0019430; P:removal of superoxide radicals; IEA.

InterPro; IPR000137; FAD_pyr_redox.

R InterPro; IPR000137; FAD_pyr_redox.

R InterPro; IPR001100; Pyr_redox.

InterPro; IPR000555; Pyr_redox.

R InterPro; IPR0065982; Thioredox_reduct.

R Pfam; PF00070; pyr_redox; 1.

R PRINTS; PR00368; FADDNR.
                                                                                                                                                                                                         de Lencastre H., wu S. W., Plino M.G., Ludovice A.M., Filipe S., Gardete S., Sobral R., Gill S., Chung M., Tomasz A.;
"Antibiotic resistance as a stress response: complete sequencing clarge number of chromosomal loci in Staphylococcus aureus strain (that impact on the expression of resistance to methicillin."; Microb. Drug Resist. 5:163-175(1999).

EMBL, Y14324, CAB82468.1;
HSSP, Q39243; lVDC.
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Pred. No. 1e-97;
0; Mismatches 2; Indels (
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 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein (Fragment).
Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                        Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR01292; TRX reduct; PROSITE; PS00573; PYRIDINE_REDOX—Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.5%;
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(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
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PRINTS; PR00469; PNDRDTASEII
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Matches 289; Conservative
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Thioredoxine reductase.
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=1280;
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SEQUENCE
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                                                                                                                          62 DLSTKMFEHAKKFGAEYQYGDIKSVEDKGDYKVINLGNKEITAHAVIISTGAEYKKIGVP 121
                                                                                                                                                                                          ORILODRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMK 242
                                                                                                                                                                                                                                                                 PLTAPEKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAA 302
                                        62
                                                                         61
                             3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                   63 DLSTKMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVP
   0; Gaps
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thioredoxin reductase.
TRXB OR BA5397.
Bacillus anthracis (strain Ames).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24, Last sequence update)
25, Last annotation update)
13;
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                                                                                      Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman M.C., Hazen A., Cline R., Redmond C., Thwaite J.E., Nierman W.C., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIG
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R GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.

R GO; GO:0019430; P:electron transport; IEA.

R GO; GO:0019430; P:emenval of superoxide radicals; IEA.

R InterPro; IPR000132; Adradx_reductase.

R InterPro; IPR000133; PyrIdine_redox_2.

R InterPro; IPR000103; PyrIdine_redox_2.

R InterPro; IPR000100; Pyr_redox_2.

R InterPro; IPR000100; Pyr_redox_2.

R InterPro; IPR000109; Pyr_redox_2.

R InterPro; IPR000193; Pyr_redox_2.

R InterPro; IPR000193; Pyr_redox_2.

R InterPro; IPR00193; Pyr_redox_2.

R PRINTS; PR00419; ADXRPIASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome's equence of Bacillus anthracis Ames and comparison to closely rome bacteria.";
Nature 423.81-86(2003).
EMBL; AE017040; AAP29046.1; -.
TIGR; BA5387; -.
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PRINTS; PR00469; PUDRDTASEII.
Probom; PUDR0139; FAD _pyr_redox; 1.
TIGREAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                   MEDLINE=22608414; PubMed=12721629;
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301 AQHYVEELLEELKT 314
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SEQUENCE 318 AA;
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Ivanova N., Sorokin A., Anderson I., Galleron N., Lapidus A.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Grou L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.;
"Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
Nature 433:87791(2003).
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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
GO; GO:0004791; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0004191; F:thioredoxin-disulfide reductase activity; IEA.
GO; GO:0018430; F:removal of superoxide radicals; IEA.
Interpro; IPR00159; FAD_pyr_reductase.
Interpro; IPR001327; FAD_pyr_redox.
Interpro; IPR00103; Pyridine_redox.
Interpro; IPR008255; Pyr_redox.
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                                                                                                                             Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=226900;
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SEOUENCE 321 AA, 34957 MW; 5B5C76F4B299D1AC CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxin reductase (EC 1.6.4.5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000139; FAD pyr redox; 1.
TIGRPAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
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RESULT

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PRT;

PRELIMINARY;

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RESULT 6 Q815J1 ID QI us-09-825-212-1.rspt

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                                                                                                                                                                                                                                                                                                                                                                                                                                      R EMBL; APD044601; BAC14425.1; -...
R GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0004791; F:thisulfide oxidoreductase activity; IEA.
GO; GO:0004791; F:thisulfide oxidoreductase activity; IEA.
GO; GO:0004791; F:thisulfide oxidoreductase activity; IEA.
GO; GO:0004791; F:thisulfide oxidoreductase activity; IEA.
R GO; GO:00041940; P:temcoval of superoxide radicals; IEA.
R InterPro; IPR000103; Pyridine_redox.
R InterPro; IPR000103; Pyridine_redox.
R InterPro; IPR000100; Pyr_redox.
R InterPro; IPR00100; Pyr_redox.
R InterPro; IPR001042; Rng_mnoxygenase.
R InterPro; IPR003042; Rng_mnoxygenase.
R InterPro; IPR003042; Rng_mnoxygenase.
R InterPro; IPR003042; Rng_mnoxygenase.
                                                                                                                                                                                                            Bacteria, Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
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                                                                                                                                                                                                                                                                                             STRAIN=HTE831 / DSM 14371 / JCM 11309,
BEDLINE=222220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Indels
                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxin reductase (NADPH) (General stress protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
A. 34337 MW, 6F0ED957848374F1 CRC64;
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                                315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERMY PFO0070; INTUINGENCALEURCE.
PERMYS; PRO0419; ADXRDTASE.
PRINTS; PR00419; PADPIN.
PRINTS; PR00419; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEI.
PRINTS; PR00420; RNGMNOXGNASE.
TIGREAMS; TIGR01292; TRX reduct; I.
PRINTS; PS005175; PYRIDINE REDOX_2; I.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 30:3927-3935(2002)
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AIKYVEDLEEKIKS 314
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                                                                                                                                                                                           Oceanobacillus iheyensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 69.1
Matches 217; Conservative
                          PRELIMINARY;
                                                                                                                                                                                                                                      NCBI_TaxID=182710;
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                                                                                                                                                      (EC 1.6.4.5).
OB2469.
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                     Q8CX98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 LRAQRILQDRAFKNDKIDFIWSHTTKSINEKDGKVGSVŢLTSTKDGSEETHEADGVEIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGTEID-FDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGEBOKVYDVVIAGAGPAGMIAAVYTSRANLSTVMVERGVPGGOMANTEDVENYPGFDH1
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
-!- COFACTOR: FAD (28:417-4331(2000)).
EMBL; AP001519; BAB07290.1; -..
PIR; C84096; C84096.
                                                                                                                                                                                                                                                                                                                                  MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reductase activity; IEA.
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GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity;

GO; GO:001619; P:electron transport; IEA.

GO; GO:0019430; P:electron transport; IEA.

InterPro; IPR001327; Par_Dyr_redox.

InterPro; IPR001327; PAT_Dyr_redox.

InterPro; IPR00130; Pyr_indine_redox.

InterPro; IPR001010; Pyr_redox.

InterPro; IPR001010; Pyr_redox.

InterPro; IPR0010342; Pyr_redox.

InterPro; IPR0010342; Pyr_redox.

InterPro; IPR0010342; Pyr_redox.

InterPro; IPR0010342; Pyr_redox.

InterPro; IPR0010342; Pyr_redox.

InterPro; IPR001042; Pyr_redox.

InterPro; IPR001042; Pyr_redox.

InterPro; IPR001042; Pyr_redox.

INTERPRO; IPR001042; Pyr_redox; I.

R PRINTS; PR00419; PNDRDTASEI.

R PRINTS; PR00420; RNGMNOXGNASE.

ITGRPAMS; TIGR01292; TRX reduct; I.

R PROSITE; PS0573; PYRIDINE REDOX.2; I.

RAD; Flavoprocein; Oxidoreductase; Complete proteome.

R PAD; Flavoprocein; Oxidoreductase; Complete Proteome.
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                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxin reductase (NADPH) (EC 1.6.4.5)
          315 AA.
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 68.6
nes 216; Conservative
                                                                                                                                                                              Bacillus halodurans.
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                                                                                                                                                                                                                                   NCBI_TaxID=86665;
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                                                                                                                                                         TRXB OR BH357;
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                               Q9K703;
Q9K703
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Complete proteome.
SEQUENCE 304 AA
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01-JUN-2003 (
01-OCT-2003 (
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Q835N8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 YGGRGVSYCAVCDGAFFRNKHVVVVGGDSAIEBGTYLTQLADKVTVIHRRDQLRAQQIL 184
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STRAIS-NCIMB 8826 / WCFS1;

STRAIS-NCIMB 8826 / WCFS1;

Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,

Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,

Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,

Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,

Riefer S.M., Nierog Groot M.N., Kerkhoven R., De Vries M., Ursing B.,

A Hoffer S.M., Nierog Groot M.N., Kerkhoven R., De Vries M., Ursing B.,

A Hoffer S.M., Nierog Groot M.N., Kerkhoven R., De Vries M., Ursing B.,

De Vos W.M., Siezen R.J.;

Complete genome sequence of Lactobacillus plantarum WCFS1.";

Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

REBL, AL93524; CAD63354.1;

COMPLETE A. OF COMPLETE A. CANGOREGUETASE ACTIVITY; IEA.

GO, GO:0015036; Frdisulfide.

GO, GO:0015036; Frdisulfide.

RINTERPRO; IPRO0137; FAD_DYI_redox.

RINTERPRO; IPRO01307; FAD_DYI_redox.

RINTERPRO; IPRO01010; PYI_redox.

RINTERPRO; IPRO01010; PYI_redox.

RINTERPRO; IPRO01109; PYI_redox.

RINTERPRO; IPRO01109; PYI_redox.

RINTERPRO; IPRO01109; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.

RINTERPRO; IPRO01104; PYI_redox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 312;
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Best Local Similarity 55.5%; Pred. No. 4.9e-59;
Matches 171; Conservative 54; Mismatches 83; Indels
                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thioredoxin reductase (NADPH) (EC 1.6.4.5).
TRYB1 OR LP_0761.
Lactobacillus plantarum.
Bacteria, Firmicutes, Lactobacillales, Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0573; PYRIDINE REDOX 2; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 312 AA; 33455 MW; BF013DD361EDB343 CRC64;
                                                                                                                                                                                           312 AA
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00010; pyr_redox; 1.
PRINTS; PR00419; ADXBDTASE.
PRINTS; PR00368; FADDNR.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
PRINTS; PR00469; RNGMNOXGNASE.
                                         301 NVQHYIEELAEKVKN 315
        300 SAAEYIEHLNDQARS 314
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                            RESULT 9
                                                                                                                                                                           288YJ7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 KMYENVEKFGTENAYGIVMGIEDHGSYKEVICDDKSYEAKAVIIATGCEHRKLGVKGEEE
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                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R EMBL; ARG16951; AA081129.1; -.

R TIGR; EF1338; -.

R GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:00015737; C:cytoplasm; IEA.

GO; GO:000191; F:thioredoxin-disulfide reductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

R GO; GO:0019430; P:electron transport; IEA.

R GO; GO:0019430; P:electron transport; IEA.

R InterPro; IPR001327; FAD pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

INTERPRO; IPR0018255; Pyr_redox.

INTERPRO; IPR0018255; Pyr_redox.

INTERPRO; IPR0018255; Pyr_redox.

INTERPRO; IPR0018255; Pyr_redox.

INTERPRO; IPR0018255; Pyr_redox.

INTERPRO; IPR0018255; Pyr_redox.

INTERPRO; IPR005982; Thioredox_reduct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-V583 / ATCC 700802;
MEDLINE-22550857; PubMed=12663927;
MEDLINE-22550857; PubMed=12663927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Bennan M., Nelson W Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                            304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00070; Pyr_redox; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00461; FADPR.
PRINTS; PR00461; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
PLODOM; PD000139; PAD_Pyr_redox; 1.
PTGRFAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                  Thioredoxin reductase.
307 HLNDQARS 314
                                                        305 ALGDKVNN 312
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Streptococcus.
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Q8K6D2;
                                                                                                                                                                                                                                                                                                          RESULT 12
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                                                       247 PFKDLGIINDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
182 QDRAFANEKISFVWDTVVEEIVGNEMVVTGVKARNVKTDEVSEIEANGVFIYVGLDPLTE 241
                                                                                                                                  301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                       7 FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S. Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Berees S.B., Campbell D.S., Smith T.M., Zhang Q., "Rapur V., Daly J.A., Veasy L.G., Musser, M., "Genome sequence and comparative microarray analysis of serotype MIS group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L PUCC. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

R EMBL; AB010078; AAL98210.1; -...

GO:00015073; C:0ytoplasm; IEA.

GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO:0019439; F:thioredoxin-disulfide reductase activity; IEA.

R GO:0019430; P:thioredoxin-disulfide reductase activity; IEA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus Pyogenes (serotype M18).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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56.3%; Pred. No. 6.3e-56;
tive 49; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
TIGREAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE_REDOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00070; pyr redox; 1
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thioredoxin reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRXB OR SPYM18 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 305 AA;
                                                                                                                                                                     307 HL 308
                                                                                                                                                                                                                            EL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outbreaks.";
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                                                                                                                                                                                                                                                                                                                                                                       Q8NZY5
                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                       Q8NZY5
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA HAZAIN=SSI-1 / Serotype M3;

RA Mazadawa I., Kurchawa K., Nakata M., Tomiyasu Y., Yamashita A.,

RA HAYAShi H., Hamada S.;

RA HAYAShi H., Hamada S.;

RT Hayashi H., Hamada S.;

RT Senome of invasive Streptococcus pyogenes; a comparative analysis of S. Pyogenes SSI-1, SR370 and MGAS8332.";

RI Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RB Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RB SENOS ARMONO C.1;

RB SENOS ARMONO C.1;

RB SENOS ARMONO C.1;

RB SENOS ARMONO C.1;

RB SENOS ARMONO C.1;

RO; GO:0006142; BAC65862.1;

RG; GO:000618; P:percxidase activity; IEA.

RG; GO:000618; P:percxidase activity; IEA.

RG; GO:000618; P:percxidase activity; IEA.

RG; GO:000618; P:percxidase activity IEA.

RG; GO:0019430; P:thioredoxin-disulfide radicals; IEA.

RG; GO:0019430; P:temoval of superoxide radicals; IEA.

RG; GO:0019430; P:tremoval of superoxide radicals; IEA.

RR INTERPO; IPR00103; PyrIdine_redox_2.

BR InterPro; IPR00103; PyrIdine_redox_2.

BR InterPro; IPR00103; PyrIdine_redox_2.

BR InterPro; IPR00103; PyrIdine_redox_2.

BR RINTS; PR0041; PNDRDASEI.

BRINTS; PR0041; PNDRDASEI.

BRINTS; PR00469; PNDRDASEI.

BRINTS; PR00469; PNDRDASEI.

BR PRINTS; PR00469; PNDRDASEI.
187 ODRAFKNDKIDFIWSHTTKSINEKDGKVGSVILTSTKDGSEETHEADGVFIYIGMKPLTA 246
                                         0;
                                                                                                                                247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAABYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.W., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of a serotype M3 strain of group A Streptocophage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative thioredoxin reductase (Putative NADH oxidase/alkyl
hydroperoxidase reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus Pyogenes (serotype M3).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Indels
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PROSITE; PS00573; PYRIDINE REDOX 2; 1.
Hypothetical protein; Peroxidase; Complete proteome.
SEQUENCE 305 AA; 33543 MW; 3F947A628769EBBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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56.3%; Pred. No. 8.7e-56;
ive 49; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                           305 AA.
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOX.2 OR SPYM3_1395 OR SPS0467.
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
Matches 169; Conserv
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DLSTRMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGABYKKIGVP 122
                                                                                                                                                                                                                                        187 QDRAFKNDKIDFIWSHTIKSINEKDGKVGSVTLISIKDGSEETHEADGVFIYIGMKPLTA 246
                                       62 KMHBPLEKFGVENLYGIVTAVEDHGNFKKVLTDDNSYETKIVIIATGAKHRPLAVAGEET 121
                                                                                                                                                                                                                                                                                               182 ÓEKAFANDKVDFIMDSVVKEIKGNDLKVTNVDIENVKTGOVNNYAFGGVFIYVGLDÞVSS 241
                                                                                                                                                                                                                                                                                                                                                          247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAABYI 305
                                                                                                                                                                                                                                                                                                                                                                                           Bolotin A., Wincker P., Manger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis sp. lactis sequence of the lactic acid bacterium Lactococcus Genome Res. 11:731-755(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TEIDFDIAIIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGP
                                                                                                                                                         127 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
      KMFBHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R 60; 60:000573; C:cytoplasm; IEA.

R 60; 60:0015036; F:disulfide oxidoreductase activity; IEA.

R 60; 60:0015036; F:disulfide oxidoreductase activity; IEA.

R 60; 60:0019439; F:thioredoxin-disulfide reductase activity; IEA.

R 60; 60:0019430; P:temoval of superoxide radicals; IEA.

R 10terPro; IPR000135; Adradx reductase.

R 10terPro; IPR000137; FDD. PyT. redox.

R 10terPro; IPR001137; PyT. PyT. redox.

R 10terPro; IPR001100; PyT. redox.

R 10terPro; IPR001100; PyT. redox.

R 10terPro; IPR001193; PyT. redox.

R 10terPro; IPR001193; PyT. redox.

R 10terPro; IPR001194; PyT. redox.

R 10terPro; IPR001194; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; IPR001195; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro; PyT. redox.

R 10terPro;
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PRINTS; PR00469; PNDRDTASEII.

TIGREAMS; TIGR01292; TRX reduct; 1.

PROSTITS; PS00673; PYRIDINE REDOX 2; 1.

FRAD; Flavoprotein; Oxidoreductase; Complete proteome.

SEQUENCE 308 AA; 33894 MW; 363397A925E48267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; D86742; D86742.
HSSP; Q39243; 1VDC.
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                     67
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Q9CH02
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                                                                                                                                                                                                                                                                                                                                                          246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 PFKDLGITNDVGYIVTKDDMTTSVPGIFAAGDVRDKGLRQIVTATGDGSIAAQSAAEYIE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMFEHAKKEGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE 126
                                                                                                                                                                                                                                                                                               181
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   99
                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
                                 2 YDTLIIGSGPAGMTAALYAARSNLSVAIIEGGAPGGMNNTFDIENYPGYDHISGPELAM
                                                                                                                                                      127 LGGRGVSYCAVCDGAFFKNKRLFVIGGGDSAVEEGTFTTKFADKVTIVHRRDELRAQRIL
                                                                                                                                                                                                                                                                    QDRAFKNDKIDFIWSHTTKSINEKDGKVGSVTLTSTKDGSEETHEADGVFIYIGMKPLTA
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FDIALIGAGPAGMTAAVYASRANLKTVMIERGIPGGQMANTEEVENFPGFEMITGPDLST
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R Proc. Proc. Sci. U.S.A. 99:14434-14439(2002).

R GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0006737; Fidisulfide oxidoreductase activity; IEA.

GO; GO:0006718; Fithioredoxin-disulfide reductase activity; IEA.

R GO; GO:0006118; P:chicoredoxin-disulfide reductase activity; IEA.

R GO; GO:0006118; P:cerron transport; IEA.

R O; GO:0006118; P:cerron transport; IEA.

R InterPro; IPR001327; FAD pyr_redox.

R InterPro; IPR001010; Pyr_redox.

R InterPro; IPR001010; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.

R InterPro; IPR008255; Pyr_redox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus mutans.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ol-CCT-2003 (TrEMBLrel. 23, Last sequence update)
Ol-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative thioredoxin reductase (NADPH) (EC 1.6.4.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.1%; Score 882; DB 16; 55.2%; Pred. No. 1e-54;
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STRAIN=UA159 / ATCC 700610 / Serotype C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRO1222; TRX reduct; 1.
PROSTIE; PS0573; PYRIDINE REDOX 2; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 304 Aa; 33117 MW; CBF?BEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165; Conservative
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NCBI_TaxID=1309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-NEM316 / Serotype III;
MEDLINE-22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R GO; GO:005337; C:cytoplasm; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:00118; P:electron transport; IEA.

GO; GO:0019430; P:electron transport; IEA.

R GO; GO:0019430; P:emcoval of superoxide radicals; IEA.

R InterPro; IPR0010759; Adradx_reductase.

InterPro; IPR001137; FAD_pyr_redox.

InterPro; IPR001137; FAD_pyr_redox.

InterPro; IPR001137; Pyr_didne_redox_2.

InterPro; IPR001100; Pyr_redox_2.

InterPro; IPR005982; Thioredox_reduct.

R InterPro; IPR005982; Thioredox_reduct.

R Pfam; PF00070; pyr_redox; 1.

R PRINTS; PR00419; ADEXDITASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 304;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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PRINTS; PR00406; PNDEDTASEII.
TIGREAMS; TIGR01292; TRX reduct; 1.
TIGREAMS; TIGR01292; TRX reduct; 1.
PROSITE; PS00573; PYRIDINE REDOX 2; 1.
HYPOThetical protein; Complete proteome.
SEQUENCE 304 AA; 33123 MW; 4B6B55E55FB84E8D CRC64;
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Last annotation update)
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53.3%; Pred. No. 1.3e-52;
ive 57; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 AA
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EMBL; AL766844; CAD45929.1; -
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Mol. Microbiol, 45:1499-15
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Matches 161; Conservative
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NCBI_TaxID=216495;
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KMFEHAKKFGAVYQYGDIKSVEDKGEYKVINFGNKELTAKAVIIATGAEYKKIGVPGEQE
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